

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: May 1, 2002, 01:38:50 ; Search time 2103.63 seconds
(without alignments)
12888.008 Million cell updates/sec

Title: US-09-715-962-1
Perfect score: 2523
Sequence: 1 atgcgcaagatatgacaag.....caatcacacaagtgagtag 2523

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 11351937 seqs, 5372889281 residues

Total number of hits satisfying chosen parameters: 22703874

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:*
1: em_estfun:*
2: em_esthum:*
3: em_estin:*
4: em_estom:*
5: em_estpl:*
6: em_estba:*
7: em_estro:*
8: em_estov:*
9: em_hic:*
10: gb_est1:*
11: gb_est2:*
12: gb_hic:*
13: gb_gss:*
14: em_gss_fun:*
15: em_gss_hum:*
16: em_gss_inv:*
17: em_gss_pln:*
18: em_gss_pro:*
19: em_gss_rod:*
20: em_gss_vrt:*
21: em_gss_other:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	ID	Description
1	198.6	7.9	740	11	BG818076
2	179.6	7.1	1101	13	CRS00008A
3	175.4	7.0	450	10	AL119755
4	147.4	5.8	566	10	AU206445
5	139.6	5.5	572	11	BF530404
6	123.2	4.9	393	10	AW158263
7	122.8	4.9	859	11	BG423148
8	116	4.6	398	10	AA036134
9	115.6	4.6	611	11	X90542
10	112.4	4.5	512	10	AW049355
11	110.8	4.4	492	11	X90543
12	103.4	4.1	445	11	BI037782
1	198.6	7.9	740	11	BG818076
2	179.6	7.1	1101	13	CRS00008A
3	175.4	7.0	450	10	AL119755
4	147.4	5.8	566	10	AU206445
5	139.6	5.5	572	11	BF530404
6	123.2	4.9	393	10	AW158263
7	122.8	4.9	859	11	BG423148
8	116	4.6	398	10	AA036134
9	115.6	4.6	611	11	X90542
10	112.4	4.5	512	10	AW049355
11	110.8	4.4	492	11	X90543
12	103.4	4.1	445	11	BI037782

13	100.6	4.0	665	11	BG820975
14	99.4	3.9	335	10	AL602784
15	99.4	3.9	459	10	AL042317
16	98	3.8	952	11	BG911698
17	96	3.7	418	10	BE702435
18	93.2	3.7	399	10	AA038839
19	93.2	3.7	918	11	BF529670
20	92.8	3.7	834	10	AI134060
21	92.2	3.7	869	10	AL539611
22	92	3.6	325	11	BF932595
23	91.6	3.6	386	11	D80024
24	88.8	3.5	329	11	BF932593
25	87.6	3.5	712	10	AU218430
26	81.6	3.2	624	10	AW960962
27	79	3.1	296	11	BF950810
28	75.2	3.0	604	11	BG819622
29	73.8	2.9	315	11	BG986345
30	72.2	2.9	330	10	BE654255
31	69.8	2.8	867	13	CNS02844
32	69.6	2.8	704	11	BG773057
33	69.2	2.7	525	10	AW383370
34	68.8	2.7	443	11	BG987524
35	66.8	2.6	913	11	BF791371
36	65.2	2.6	191	11	BI039561
37	64.8	2.6	452	13	BH100127
38	64.8	2.6	599	13	BH100872
39	63.4	2.5	283	10	AA324303
40	63	2.5	1063	11	BF799281
41	62.6	2.5	483	10	AI119788
42	61.6	2.4	551	11	BF194073
43	61.2	2.4	619	10	AI404922
44	60.8	2.4	320	10	AW380854
45	60	2.4	303	10	AW380861

ALIGNMENTS

RESULT 1

LOCUS BG818076 740 bp mRNA EST 22-MAY-2001
DEFINITION 602779584F1 NCI_CGAP_Brn67 Homo sapiens CDNA clone IMAGE:4915244
5', mRNA sequence.
ACCESSION BG818076
VERSION BG818076.1 GI:14165663
KEYWORDS EST
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 740)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-re@mail.nih.gov
Tissue Procurement: David N. Louis, M.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLNL0823 row: 9 column: 21
High quality sequence stop: 735.
Location/Qualifiers
1. 740
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:4915244"
/clone_lib="NCI_CGAP_Brn67"
/tissue_type="anaplastic oligodendroglioma with 1p/19q loss"

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/lab_host="DH10B (T1 phage-resistant)"
/Note="Organ: brain; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally. Primer: Oligo dt.
Average insert size 2.3 kb. Constructed by Life
Technologies. Note: this is a NCI_CGAP Library."
BASE COUNT      187 a   194 c   193 g   166 t
ORIGIN

Query Match
Best Local Similarity 7.9%; Score 198.6; DB 11; Length 740;
Matches 430; Conservative 0; Mismatches 294; Indels 25; Gaps 3;

QY 442 cgattccaccattattccgaccattccatccgagccaggtgacaaatcccaacgcgcac 501
D 1 CGTTTCCCACTTTCTTCCGAACGACCCCATCCAGCCACACTCCACACCACTTACCCTG 60
QY 502 aagctgatgaagaaattcgctggtcccggtggccattctgcagcagcgaggagtc 561
D 61 AAACCTCTTTGAAAGAGTGGGCTGGAAGAAGATTGCTACCATCCAGCAGCAGCTGAGTC 120
QY 562 ttatattcgaccctagaggtctcgaaatcgatgcagaggtggtggtgaaatcgt 621
D 121 TTCATTCTGACTCTGGAGCAGCTGGAGGAGGAGTGAAGGAGGCTGGAAATTGAGATTACT 180
QY-- -622 actagacaatcttctatccgattcccaacagacgcctggtgcaatttgcgacgcagat 681
D 181 TTCCGCCAGAGTTCTTCTAGATCCAGCTGTCGCGTCAAAAACCTGAAGCGCCAGAT 240
QY 682 gcacgcatcttggtgactcttctatgtgtggtggtggtggtggtggtggtggtggtggt 741
D 241 GCCCGAATATCTGGGACTTTTCTATGAGACTGAAGCGCCGAAAGTTTGTGTGAGTG 300
QY 742 tacaacacagcagctatgtggtggtggtggtggtggtggtggtggtggtggtggtggtggt 801
D 301 TACAAGGAGCGCTCTTTTGGGAGAAAGTACGTCTGGTTCCTTCATTTGGTGGTGTATGCTGAC 360
QY 802 aactggttacgaggtgaaatctgaaagcagagggcgcacactgctggtgaaacagatcga 861
D 361 AATTGTTCAAGATCTACGACCCCTTC-----TATCAACTGCACAGTGATGAGTACT 414
QY 862 atagctgccgaagacatctgacacggaagcgctcatgtggaatcagaacaatcagaca 921
D 415 GAGCGGTGAGGCGCCACATCACAACTGAGATTGTCATGCTGTAATCTCTGCCAATACCCGC 474
QY 922 actatattccggaatgactgagaggaatttcgacatcgactgaatcagcgctaatcag 981
D 475 AGCATTTTCCAACTGACATCCAGGAATTTGTGGAGAAACTTAACCAAGCGACT----- 527
QY 982 gaggggtacgacattacccagatcgctatccgagggatcagagggcgcacactgccc 1041
D 528 -----GAAAGACACCTTGAGGAGACAGAGGCTTCCAGAGGACCGCTGGCC 576
QY 1042 tagatgagtgagtggtggtggtggtggtggtggtggtggtggtggtggtggtggtggtggt 1101
D 577 TATGATGCCATCTGGGCTTGGCACTGGCCCTGAACAGACATCTGGAGGAGGCGGCGCTT 636
QY 1102 ggaagaatactctgagggattttacattatcaggaagagagattgcccgtgaaatctac 1161
D 637 CTGGTGTGCGC-CTGGAGGAGTTCAACTTACAACAACACAGACCATTAACCGACCAATCTC 695
QY 1162 gctgccaatgaactccacaaatttctggg 1190
D 696 CGGCAATGAATCTCTCTGCTCTTTGAGGG 724

RESULT 2
LOCUS      CNS000BA      1101 bp      DNA      03-JUN-1999
DEFINITION Drosophila melanogaster genome survey sequence TET3 end of BAC #
            BACR01C07 of RPCI-98 library from Drosophila melanogaster (fruit
            fly), genomic survey sequence.
ACCESSION  AL063634
```

```
VERSION      AL063634.1      GI:4938682
KEYWORDS     GSS.
SOURCE       fruit fly.
ORGANISM     Drosophila melanogaster
             Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
             Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
             Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
REFERENCE    1 (bases 1 to 1101)
AUTHORS      Genoscope.
TITLE        Direct Submission
JOURNAL      Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage :
             BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr)
             - Web : www.genoscope.cns.fr)
COMMENT      Determination of this BAC-end sequence was carried out as part of a
             collaboration with the Berkeley Drosophila Genome Project (BDGP).
             The BDGP is constructing a physical map of the Drosophila
             melanogaster genome using these BACs. For further information
             please see http://www.fruitfly.org The BDGP Drosophila
             melanogaster BAC library was prepared by Kazutoyo Osoegawa and
             Aaron Mammosser in Pieter de Jong's laboratory in the Department of
             Cancer Genetics at the Roswell Park Cancer Institute in Buffalo,
             NY. The library is named RPCI-98 and was constructed by partial
             EcoRI digestion of Drosophila DNA provided by the BDGP from the
             isogenic strain Y2; cn bw sp, the same strain used for the BDGP's
             p1 and EST libraries. A more detailed description of the library
             and how to order individual BAC clones, the entire library, or
             filters for hybridization from the BACPAC Resource Center can be
             found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
FEATURES     Location/Qualifiers
             source          1..1101
             /organism="Drosophila melanogaster"
             /db_xref="taxon:7227"
             /clone_lib="RPCI-98"
             /clone="BACR01C07"
             /note="end : TET3"
BASE COUNT   303 a   206 c   209 g   361 t   22 others
ORIGIN

Query Match      7.1%; Score 179.6; DB 13; Length 1101;
Best Local Similarity 99.0%; Pred. No. 2.4e-40;
Matches 190; Conservative 1; Mismatches 0; Indels 1; Gaps 1;

QY 2332 cagaagagagaaattcgaatcctcgcacagcgtctgtagcgagcgagcgagcgaag 2391
D 2332 cagaagagagaaattcgaatcctcgcacagcgtctgtagcgagcgagcgagcgagcgaag 2391
QY 349 CAGAAGAGGAAAGATTGAGTCTTCCGACA-SGTCTGTGTGGAGCGGGCGAGCGCAAG 407
D 349 CAGAAGAGGAAAGATTGAGTCTTCCGACA-SGTCTGTGTGGAGCGGGCGAGCGCAAG 407
QY 2392 ggacagaactgaattgtgcaacaggtgtcgctccgcgcgcgttgcacaactctcgag 2451
D 2392 ggacagaactgaattgtgcaacaggtgtcgctccgcgcgcgttgcacaactctcgag 2451
D 408 GGCACAGAACTGAATGTGTCAACAGGTGTGCTCTCCGCGCGCTTGCACAACTTCCGAG 467
QY 2452 cccgttccctcatcaactcatcagcacatgccacgcgcgcgcagccacactcgaatcaca 2511
D 2452 cccgttccctcatcaactcatcagcacatgccacgcgcgcgcagccacactcgaatcaca 2511
D 468 CCGCGTTCCTCATCAACTCATCAGCACATGCCACGCGCGCGAGCCACACTTCCGAATCACA 527
QY 2512 caagtgatag 2523
D 2512 caagtgatag 2523
D 528 CAAGTGTAGTAG 539

RESULT 3
LOCUS      AL119755
DEFINITION DKFZp761C0724_r1 761 (synonym: hamy2) Homo sapiens cDNA clone
            DKFZp761C0724 5', mRNA sequence.
ACCESSION  AL119755
VERSION    AL119755.1      GI:5925654
KEYWORDS   EST.
SOURCE     human.
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE  1 (bases 1 to 450)
```

AU206445
AU206445.1 GI:14839613
EST.
Caenorhabditis elegans.
Caenorhabditis elegans.

Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea; Rhabditidae; Palodirinae; Caenorhabditis.

1. Kohara, Y., Shin-I, T., Thierry-Mieg, J., Thierry-Mieg, D., Suzuki, Y., and Sugano, S. A complementary view of the *C. elegans* genome (Unpublished (2001)).

Contact: Yutii Kohara

Genome Biology Lab.
National Institute of Genetics
Yata 111, Mishima, Shizuoka 411, Japan
Tel: 81-559-81-6854

Fax: 81-559-81-6855
Email: ykohara@lab.nig.ac.jp.
Location/Qualifiers
1. .566
/organism="Caenorhabditis elegans"
/strain="N2"
/db_xref="taxon:6239"
/clone="yk864d02"
/clone_lib="unpublished oligo-capped cDNA library stage

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/clone_r11b= unpublished cargo capped cDNA library; stage
L1"
/sex="Hermaphrodite"

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```

/tissue_type="whole animal"
/dev_stage="L1"
154 a      116 c      130 g      165 t      1 others

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h 5.8%; Score 147.4; DB 10; Length 566;
Similarity 57.9%; Pred.No. 3.9e-31;
81: Conservative 0; Mismatches 201; Indels 3; Gaps 1;

gagcgTgcggcggaggcccgatgaactgcacatcgccgatcttccgat---agcc 138
| | | | | | | | | | | | | | | | | | | | |
GTGGGCTTCGGCCGAGCCGTCACCTTCACATCGGTGGCAGTTCCGATGGAACT 136

caaaagagatgcaggcgccgagtgtatgcctgccacaagaactggcgttgat 198
| | | | | | | | | | | | | | | |
| | | | | | | | | | | | | | | |
CTCCGGAGGATGGCAGGAGGACGCATGTCTCCGGCACTTCAGATGCCACTGAA 196

tgtcaacagcagccgaatgctgcggcggtctcaagctcatcctgcacagcaacgac 258
||||| — ||||| ||||| ||||| ||||| ||||| ||||| |||||
TGTCATATAGTCGATTAGATATTCTACCTGGTAGGTACTTAAATGACTAATCACAC 256

cgaagtgtgagcccggtttggggcccgcgtgatgtacaatctgctctataataaacgcg 318
||||| |||| | ||| ||| ||| ||| ||| ||| |||
GCAGTGTCAACCAGGTCCTCTATGCAACAAATTATGATGATTTCTTTATAACCCACT 316

aagctgtagctgttgccaggatgcagcagcgctgcaccacitgaqccaggagtgc 378
||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
GAGCTGTAGTCTTCAACAGGATGTAGTCGGTCACAACITGAATTGCTGAAGCTGG 376

aatgtggaatactaaattgtcctctgcacagggcgctcagagtccggactcttcgggatcgc #38
||||||| ||| ||||| | ||||| ||| ||||| ||| ||||| |||
AGTGTGGAAACCTAGTTGTTATCATACGGTGGGAAGCTTCCTGCACATTTCCAATAGA #36

acgattccccactctattccgcacccatccatcgccacgggtgcacaaatcccaacgccc 498
||||||| || ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
TCGATTCCCAACATTGTTAGGACTCACCGTCAGCGAATATCGAGAACCCACGCCGA 496

caagctgtagaagaataatcgctgtgtcccggttgccattctgcagcagcgaggaggg 558
| | | | | | | | | | | | | | | | | | | | |
TCACATAATGGGAAAAATTCAATGGAAAGATTACTATTGTGCGGTTGAGGAA 556

ctt 563
||
ttt 561

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RESULT 5
BF530404 572 bp mRNA EST 11-DEC-2000
LOCUS 602071520F1 NCI_CGAP_Brn67 Homo sapiens cDNA clone IMAGE:4214429
DEFINITION 5', mRNA sequence.
ACCESSION BF530404
VERSION BF530404.1 GI:11617767
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 572)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs@mail.nih.gov
Tissue Procurement: David N. Louis, M.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM9788 row: g column: 06
High quality sequence stop: 571.
FEATURES
Location/Qualifiers
1..572
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:4214429"
/clone_lib="NCI_CGAP_Brn67"
/tissue_type="anaplastic oligodendroglioma with lp/19q
loss"
/lab_host="DH10B (T1 phage-resistant)"
/notes="Organ: brain; Vector: pCMV-SPORT6; Site 1: NotI;
Site 2: SalI; Cloned unidirectionally. Primer: Oligo dt.
Average insert size 2.3 kb. Constructed by Life
Technologies. Note: this is a NCI_CGAP Library."
BASE COUNT 144 a 140 c 164 g 124 t
ORIGIN

Query Match 5.5%; Score 139.6; DB 11; Length 572;
Best Local Similarity 56.5%; Pred. No. 6.9e-29;
Matches 315; Conservative 0; Mismatches 219; Indels 24; Gaps 2;

QY 535 gccatttcgacgagcgaggaggtctttatctatcgcgtagagcgtagagatctcgagaatcga 594
DB 13 GCTACCATCCAGCAGACACCTAGGCTCTTCACTTCGACTCTGGAGACCTGGAGGAACGA 72
QY 595 tgcattgaggtggcgttgaaatcgtacatagacaatcattctatccgatcccaacagac 654
DB 73 GTCAAGGAGGCTGGAATTGAGATTACTTTCGCCAGAGATTCTCTCAGATCCAGCTGTG 132
QY 655 gccgtgcgaatttgacgccagagatgcagcatcattgtggagactctctatgtggtg 714
DB 133 CCGCTCAAAAACCTGAAGGCCAGGATGCCGGAATCGTGGGACTTTGTCTGAGACT 192
QY 715 gccgcagaggggtgctctcgaaatgatacaaacagcagctatattgcccgcgtcatgtg 774
DB 193 GAAGCCCGGAAGTTTTTTGTGAGTGCTACAGGAGCGTCTCTTTGGGAAGAAGTACGTC 252
QY 775 tgggtctttattggcttgacgaggaacactgtgtacgaggtgaaatctgaaagcagagggc 834
DB 253 TGGTCTCTCATTTGGTGGTGTGCTGACAAATGGGTTCAGATCTACGACCCCTTC-----T 306
QY 835 atcacctgcactgttgaaacagatgcgaatagctgcgaagacatctgacacaggaagcg 894
DB 307 ATCAACTGCACAGTGGATGATGACTGAGGCGGTGGAGGCCACATCACAACTCGAGATT 366

```

```

QY 895 ctcatgtggaatcagaacaactatccggaatgactgcagaggaatttga 954
DB 367 GTCATGCTGAATCTCTGCCAATACCCGCGAGCATTTCCAACATGACATCCAGGAATTTGTG 426
QY 955 catcgaactgaatcagcgctctaatacagagggttacacattaaacacagatcgctatccg 1014
DB 427 GAGAAACTAACCAAGCGACT-----GAAAAGACACCTCGAGGAGACA 468
QY 1015 gaggaatatcagagggcgccactcgcctacgatgcagtggtgagtgcttggctttc 1074
DB 469 GGAGCTTCCAGGAGCGACCGCTGCCTATGATGCATCTGGCCCTTGGCACTGGCCCTG 528
QY 1075 aacaagaccatggaacga 1092
DB 529 AACAGACATCTGGAGGA 546

RESULT 6
AW158263 393 bp mRNA EST 05-NOV-1999
LOCUS 2a39b08.xl Xenopus EST library Xenopus laevis cDNA clone 2a39b08
DEFINITION 5', mRNA sequence.
ACCESSION AW158263
VERSION AW158263.1 GI:6270292
KEYWORDS EST.
SOURCE African clawed frog.
ORGANISM Xenopus laevis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipiloidea; Pipidae;
Xenopodinae; Xenopus.
REFERENCE 1 (bases 1 to 393)
AUTHORS Schutz,K., de la Bastide,M., Huang,E.N., Nasclmento,L., Preston,R.,
Shah,R., Swaby,I., Shekher,M., Spiegel,L., Vil,M.D. and McCombie
,W.R.
TITLE Expressed sequence tags from Xenopus
JOURNAL Unpublished (1999)
COMMENT Contact: W. Richard McCombie
Lita Annenberg Hazen Genome Sequencing Center
Cold Spring Harbor Laboratory
PO Box 100, Cold Spring Harbor, NY 11724, USA
Tel: 516 367 8884
Fax: 516 367 8874
Email: mcombie@cshl.org
Plate: 2a39 row: b column: 08
Seq primer: M13 universal forward primer
High quality sequence stop: 393.
FEATURES
Location/Qualifiers
1..393
/organism="Xenopus laevis"
/db_xref="taxon:8355"
/clone="2a39b08"
/clone_lib="Xenopus EST library"
/tissue_type="total brain tissue"
/dev_stage="W22-TGA"
/dev_stage="tadpole"
/notes="Vector: Lambda Zap I; Site 1: XbaI; This library
was supplied by Holly Cline (Cold Spring Harbor Labs).
cDNA synthesis with oligo dt Xba I (Xba I cloning site).
RNA: stage 50-56 tadpoles, total brain tissue, GTC
extraction method."
BASE COUNT 94 a 98 c 91 g 110 t
ORIGIN

Query Match 4.9%; Score 123.2; DB 10; Length 393;
Best Local Similarity 58.9%; Pred. No. 3.3e-24;
Matches 231; Conservative 0; Mismatches 158; Indels 3; Gaps 1;

QY 1745 cttggaagctatacacccatggttctggggtctattatcaatagatttagtattactct 1804
DB 1 CATGGAAGCTCTACACTACAGTCTCACTTTTGTGGCGCTGGATGTCATAACACTAGGGA 60

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Qy 1805 catggcagatcttggatccgctgacgctgtatctcgaacattcccaactcgaagatccag 1864
 Db 61 TCTGGCAGATAGTGGACCCCTACACGGTCTCTATTGAGGAATTTACCAAGAAAGAACTC 120
 Qy 1865 tatctactactgatattataaatacgtccagagcttgagcattgtgaagtcgaacgca 1924
 Db 121 GTGGTGACCTGGATGTCTC--ATACTCCGCGAGCTGGAACTGCACTGCAGTCTCTCAAGA 177
 Qy 1925 actcaatgctgggtgctgtgtatatacggcttcgaagggttaactcgtgtgttggcctct 1984
 Db 178 TGAACACATAGGCTGTGTATAGTATATAGTCTCTAAAGGGCTACTCCTTTTGGTGTATAT 237
 Qy 1985 ttttggctaccagacgctgcattaaagtgaacagatcaacagattcgcgttatatgg 2044
 Db 238 TCTTGCCCTATGAGCAAGAGTGTCTCACTGAGAGATCAATGACCCAGCTGCTGTGG 297
 Qy 2045 gcatgagcatcataacgtggtgctgctcttggctgtataacagctccggtgggcatgtca 2104
 Db 298 GGATGCTATATACATGTGGCTGTCTTTGGCTCTATCACCCTCCAGTCAATGATGATCC 357
 Qy 2105 ttgcacgcgaacaggcgcgtcctttgcttc 2136
 Db 358 TCAGTAGCCAGCAGGACGCTTCTTTGCATTC 389

RESULT 7

BG423148 859 bp mRNA EST 14-MAR-2001
 LOCUS 602450359F1 NIH_MGC_14 Homo sapiens cDNA clone IMAGE:4588791 5',
 mRNA sequence.

ACCESSION BG423148
 VERSION BG423148.1 GI:13329654
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 NIH-MGC http://mgc.nci.nih.gov/.
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-r@mail.nih.gov
 Tissue Procurement: DCTD/DTF
 cDNA Library Preparation: Ling Hong/Rubin Laboratory
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 http://image.llnl.gov
 Plate: LLCMI321 row: e column: 16
 High quality sequence stop: 729.
 Location/Qualifiers

FEATURES
 source
 1..859
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 /db_xref="taxon:9606"
 /clone="IMAGE:4588791"
 /clone.lib="NIH_MGC_14"
 /tissue_type="renal cell adenocarcinoma"
 /lab_host="DH10B (phage-resistant)"
 /note="organ: kidney; Vector: pOTB7; Site_1: xhoI; Site_2:
 EcoRI; cDNA made by oligo-dT priming. Directionally
 cloned into EcoRI/XhoI sites using the following 5'
 adaptor: GGACGAC(G). Size-selected >500bp for average
 insert size 1.8kb. Library constructed by Ling Hong in
 the laboratory of Gerald M. Rubin (University of
 California, Berkeley) using ZAP-cDNA synthesis kit
 (Stratagene) and Superscript II RT (Life Technologies)."

BASE COUNT 215 a 219 c 260 g 165 t

Query Match 4.9% Score 122.8; DB 11; Length 859;

Best Local Similarity 52.1%; Pred. No. 5, 2e-24;
 Matches 321; Conservative 0; Mismatches 292; Indels 3; Gaps 2;
 Qy 1705 acaacaagaacaaactgacccaaagaaaaaacttggaaccttggaagctatacaccatg 1764
 Db 4 AGAAGGAAGAAAGAGAGTGGAGGAAGACTCTGGAAACCTTGGAAAGCTGTATGCCACA 63
 Qy 1765 gtttcggggctattataatagatttagtattactctcatggtcagatctttgcatcgg 1824
 Db 64 GTGGCCCTGCTGGTGGGATGGATGCTCTACTCTCGCCATCTGGCAGATCTGGACCT 123
 Qy 1825 ctgcaagcttatctcgaacattcccaactcgaagatccagatctactactactatatt 1884
 Db 124 CTGCACCGGACCATTTGACACATTTGCCAAGGGAGGAACCTTAGGAGATAT--TGACGTC 181
 Qy 1885 aaaaactcgcagagcttgagcattgtgaaagtcaacccaactccatcgtggttgggtct 1944
 Db 182 TCTATTCTGCCCCAGCTGGAGCATTCGAGCTCCAGGAAGATGAATACATGGCTTGGCATT 241
 Qy 1945 gtatacggcttcaaggggtaactcctggtgttggcctctttttggtacgagacgcg 2004
 Db 242 TTCTATGTTTACAGGGGCTGCTGTGCTGTGGAAATCTTCTTCTTATGAGACCAAG 301
 Qy 2005 tccattaaagtgaacagatcaacgattcgcgttatgtgggcatgagcatctataacgtg 2064
 Db 302 AGTGTCTCCACTGAGAAGATCAATGATCACCGGCTGTGGGCATGGCTATCTACATATGTG 361
 Qy 2065 gtcgctcttgcctgataacagctccggtgggcatggtcattgcatcgcaacagacgcg 2124
 Db 362 GCAGTCTCTGCTCATCTACTCTCTGTCCACCATGATCTGTCCAGCCAGGATGCA 421
 Qy 2125 tcccttgctcgttgcctagctgtgatatctgttcttcttaagcatgtctgtgata 2184
 Db 422 GCTTTGCTTGTGCTCTCTTGGCATAGTTTCTCTCTCTCTATATACATCTCTGTG-TGCTC 480
 Qy 2185 tttgtgcaaaaggtcattgaggttatacgtcatcccaaggataaagcgaatcgaataat 2244
 Db 481 TTTGTGCCCAAGATGCGCAGGCTGATACCCCGAGGGAATGGCAGTCGGAGCGCAGGAC 540
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 Db 541 ACCATGAACAGAGGTCATCGAGCAACACACAGAGGAGGAGAGTCCCGGCTGTGGAG 600
 Qy 2305 aacgagcaattgcaac 2320
 Db 601 AAAGAGAACCCTGAAC 616
 RESULT 8
 AA036134/c
 LOCUS mi75a09.r1 Soares mouse p3NMF19.5 Mus musculus cDNA clone 26-AUG-1996
 DEFINITION IMAGE:472408 5', mRNA sequence.
 ACCESSION AA036134
 VERSION AA036134.1 GI:1509324
 KEYWORDS EST.
 SOURCE house mouse.
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 REFERENCE 1 (bases 1 to 398)
 AUTHORS Garra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
 Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
 Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
 Theising,B., Wylie,F., Lennon,G., Soares,B., Wilson,R. and
 Waterston,R.
 TITLE The WashU-HMI Mouse EST Project
 JOURNAL Unpublished (1996)
 COMMENT Contact: Marra M/Mouse EST Project
 WashU-HMI Mouse EST Project
 Washington University School of MedicineP
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
 Tel: 314 286 1800

```

Fax: 314 286 1810
Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
MGI:283152
Seq primer: -28M13 rev2 from Amersham
high quality sequence stop: 371.
Location/Qualifiers
1. .398
/organism="Mus musculus"
/db_xref="taxon:10090"
/clone="IMAGE:472408"
/clone_lib="Soares mouse p3NMFL9.5"
/dev_stage="19.5 dpc total fetus"
/lab_host="DH10B (ampicillin resistant)"
/note="Vector: pT73D (Pharmacia) with a modified
polylinker; Site_1: I; Site_2: Eco RI; 1st strand cDNA
was primed with a Not I - oligo(dT) primer [5',
TGTTACCAATCTCAAGTGGGAGCGCGCATTTTTTTTTTTTTTTT 3'],
double-stranded cDNA was size selected, ligated to Eco RI
adapters (Pharmacia), digested with Not I and cloned into
the Not I and Eco RI sites of a modified pT73 vector
(Pharmacia). Library went through one round of
normalization to a Cot = 5. Library constructed by Bento
Soares and M.Fatima Bonaldo. RNA was kindly provided by
Dr. Minoru Ko (Wayne State University)."
100 a 91 c 118 g 89 t

```

REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 611)
AUTHORS	Totaro,A., Rommens,J.M., Grifa,A., Lunardi,C., Carella,M., Huizenga,J.J., Roetto,A., Camaschella,C., De Sandre,G. and Gasparini,P. Hereditary hemochromatosis: generation of a transcription map within a refined and extended map of the HLA class I region Genomics 31 (3), 319-326 (1996)
TITLE	
JOURNAL	
MEDLINE	96435427
COMMENT	Contact: P. Gasparini Medical Genetics Service Hospital, I.R.C.C.S. 'CASA Soll. Sofferenza' Viale Cappuccini, 71013 San Giovanni Rotondo, Foggia, ITALY.
FEATURES	Location/Qualifiers
source	1. 611 /organism="Homo sapiens" /db_xref="taxon:9606" /map="6p21.3" /clone="GT 545" /clone.lib="Human PGasparini"
BASE COUNT	159 a 150 c 174 g 126 t 2 others
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Query Match	4.6%; Score 115.6; DB 11; Length 611;
Best Local Similarity	51.0%; Pred. No. 5.8e-22;
Matches 294: Conservative	0; Mismatches 281; Indels 1; Gaps 1;

Query Match	4.6%	Score 116;	DB 10;	Length 398;
Best Local Similarity	56.6%	Pred. No. 4e-22;		
Matches 215;	Conservative 0;	Mismatches 165;	Indels 0;	Gaps 0;
QY 1114	ctgaggatattac	tatcgcacaggaatgcccatgataaatactacgctgcgcataaac	1173	
DB 382	CTGAGGACCTTAACTACAAACACACACATTTACAGACCAAAATCTACCGGGCCATGAAC	323		
QY 1174	tccacacaatttcgggtgatccgggtgtggtgcattcagttcttcaggggcgatcgctatt	1233		
DB 322	TCCTCCTCCTTGAGGGTGTTCTTGCCACAGTGCTTC	263		
QY 1234	gctottacacagatcgcacagatgatagacgcgaagtacgagaagttgggttactacgat	1293		
DB 262	GCATGGACGGCTTATCGAGCAGCTACAGGGCGGACGTACAGAAGATCGGCTAGTACGAC	203		
QY 1294	actcagttggataacacctatcctcgtgtgaatactagacagtgattgtgtgcgaaggtctct	1353		
DB 202	AGCACCAAGGATGATCTTCTGTGTCCTCAAAACACACAAAGTGGATCGGAGGCTCTCCGCCA	143		
QY 1354	caagatcgcacaaattgtocaccatgtttctacgcaccgtgtccttgccattatttgtgtgc	1413		
DB 142	GCCGACACGACCTTGGTCATCAACACATATTCGGTTTCCTGTGCACAGAAACTCTTTATCTCC	83		
QY 1414	atgtgcacaatatccagtttggcatatttggttgccttcgccttgatcatctttaata	1473		
DB 82	GTCTCAGTTCTCTCCAGCCTGGGATTTGTTCTGTGTCTGTCTGCTTCTTTAAACATC	23		
QY 1474	tggaaatgaagcatagaagagt	1493		
DB 22	TACAACTCCCACACTTCAGATT	3		

[illegible]

RESULT	9	
X90542/c		
LOCUS	X90542	611 bp mRNA
DEFINITION	HSGT545 Human PCasparini Homo sapiens	EST 20-MAY-1996
	sequence.	cdna clone GT 545, mRNA
ACCESSION	X90542	
VERSION	X90542.1	GI:1296643
KEYWORDS	EST.	
SOURCE	human.	
ORGANISM	Homo sapiens	

RESULT	10					
AW049355/c						
LOCUS	AW049355	512 bp	mRNA	EST	18-SEP-1999	
DEFINITION	IIT-W-BH1-ane-a-07-0-II	s1	NTH BMAP M S2	Mus musculus cDNA clone		


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/lab_host="DH10B (T1 phage-resistant)"
/notes="Organ: brain; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally. Primer: Oligo dt.
Average insert size 2.3 kb. Constructed by Life
Technologies. Note: this is a NCI_CGAP Library."
155 a 186 c 147 t
BASE COUNT

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Query Match	4.08;	Score 100.6;	DB 11;	Length 665;
Best Local Similarity	51.0%;	Pred. No. 1.2e-17;		
Matches 289;	Conservative 0;	Mismatches 274;	Indels 4;	Gaps 2;
QY 1803	ctcatgacagatcttggatccgctgcagcgttatctcgaaacattcccaatccgaagatcc	1862		
Db				
2	CACCGCTCCGATCGTGACCCCTCGACCGGACCATTTGAGACATTTGCCAAGGAGGAACC	61		
QY 1863	agtatctactactgatataataaacgtccagagcttgagcattgtgaaagtcaacg	1922		
Db				
62	TAAGGAAGATATTGACG--TCTCTATTTCGCCCCAGCTGGAGCATTCGAGTCCAGGAA	118		
QY 1923	caactccatgtggttggtctgtatcaggcttcaaggggttaactctgtgtgttgacct	1982		
Db				
119	GATGAATACATCGGCTGGCATTTTCTATGTGTACAAAGGGGCTGCTGCTGCTGGGAAT	178		
QY 1983	cttttggcgctacgagacgcgctccattaaagtgaacagatcaacgattccgcttat-g	2041		
Db				
179	CTTCCTTTGCTTATGAGACCAAGAGTGTCTCCATGAGAAAGATCAATGATCACCGGGCTAG	238		
QY 2042	tgggcatagagcatctaaacgtggctgcgtctctttgcttgataacagagctccggtgggcattg	2101		
Db				
239	TGGCATGGCTATCTACAAATGTGGCAGTCTGTGCCATCAGTCTCTGTCCACATGA	298		
QY 2102	tcatgtcatcgcaacaggaagcgtcccttggctcgttgcctcagctagctggtgatattcgtt	2161		
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299	TTCTGTCCAGCCAGCAGATGCAGCGCTTGCTTTGGCTCTCTTTGCCATAGTTTTCCT	358		
QY 2162	gtttccctaaagcatgctgctgatatttggccaaaggtcattgaggttatcagtcctatccca	2221		
Db				
359	CCATATACATCTTTGATGCTCTTTGTGCCCAAGATCCGAGGCTGATCACCCGAGGGG	418		
QY 2222	aggaataagggcgaatcgaataacaaatcccgattccagccatatacgaaagagacgaagaac	2281		
Db				
419	AATGGCAGTCGGAGGGCGAGACACCATGAAGACAGGGTCTATCGACCAACAAACACGAGG	478		
QY 2282	gctatcgaaactgttaccgaaacagcgaatgtcaacgatttaataaacacagaagagag	2341		
Db				
479	AGGAGAAGTCCCGCTGTTGGAGAAGAGAACCGTGAACTCGACCATCATTTCTCTGAGA	538		
QY 2342	aaaagattcgagtcctgcacagcgtc	2368		
Db				
539	CAGAGAGCGTGTCTCTGAACCTGGCC	565		

RESULT	14
AL602784	
LOCUS	335 bp mRNA EST 14-AUG-2001
DEFINITION	DKFZP686J21116_r1 686 (synonym: h1cc3) Homo sapiens cDNA clone
ACCESSION	KF295687J21116 5' mRNA sequence.
VERSION	AL602784
KEYWORDS	AL602784.1 GI:15166290
SOURCE	EST.
ORGANISM	human.
REFERENCE	Homo sapiens
AUTHORS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi
TITLE	Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
JOURNAL	1 (bases 1 to 335)
COMMENT	Wambutt R., Heubner D., Mewes W., Weil B. and Wiemann S. EST (Wambutt R., Heubner D., Mewes H.W., Weil B. and Wiemann S.) Unpublished (1999) Contact: Wambutt R MIPS Am Klopferspitz 18a D-82152 Martinsried, Germany

This is the 5' sequence of the clone insert
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;
sequenced by AGOWA (Berlin/Germany) within the cDNA sequencing
consortium of the German Genome project.

This clone (DKFzp686j2116) is available at the RZPD in Berlin. Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059 Berlin-Charlottenburg, GERMANY; Email: clone@rzd.de

FEATURES
SOURCE

BASE COUNT
ORIGIN

Query Match
Best Local
Matches

Qy	1000	cacga tcgctatccggaggga taccgaagcgcccaactcgcctacgatcgagtgtggagt	1059
Db	11	CACCCTGAGGACACAGAGGGCTTCGACGAGGCACCGCTGGCCTATGATGCATCTGGCC	70
Qy	1060	gtggcttggctttcaacaagaccatgaaacgattgacaaaccggagaagaatactctgagg	1119
Db	71	TTGGCACCTGGCCCTGAACAAGAACAATCTGGAGAGGCGGCCCTTCTGTGTGGCCTGGAG	130
Qy	1120	gattttacctatcacgacaagagattgccatgaaatctctacgctgcgaatgaactccaca	1179
Db	131	GACTTTCAACTACAAACAACAGACCACTATTCCGACCAAATCTACCGGGCAATGAACCTCTTCG	190
Qy	1180	caattctcgggtgatatcgggtgtgtggcatctcagttctcaggcgcatcgtattgctctt	1239
Db	191	TCCTTTGAGGGTGTCTCTGGCCATGTGGTGTGTTGATGCCACGGGCTCTCGATGGCATGG	250
Qy	1240	acacagatcgaacagatgatagacgcgaagtacgagaagtgttggttactacgatactcag	1299
Db	251	ACGCTTATCGAGCAGCTTCAGSGTGGCAGCTACAAGAAGATTGGCTACTATGACAGCAC	310
Qy	1300	tbggataacctatcctggttgaata	1324
Db	311	AAGGATGATCTTTTCTGGTCCAAAA	335

RESULT 15
AL042317

LOCUS	DEFINITION	EST	EST	EST
AL004231.7	AL004231.7	459 bp	mrna	29-FEB-2000
	DEFINITION			
	DKFZP434N0320_r1.434 (synonym: htes3)		Homo sapiens	cdna clone
	FFP434N0320 5', mRNA sequence.			
	ACCESSION			
	AL004231.7			
	VERSION			
	AL004231.1	GI:5421659		
	KEYWORDS			
	EST.			
	SOURCE			
	human			

SOURCE
ORGANISM

REFERENCE	AUTHORS	TITLE	JOURNAL	COMMENT
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MIPS
Am Klopferspitz 18a D-82152 Martinsried, Germany

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: May 1, 2002, 01:49:00 ; Search time 101.45 seconds
(without alignments)
5632.371 Million cell updates/sec

Title: US-09-715-962-1

Perfect score: 2523

Sequence: 1 atgcgcaagatatacaag.....caatcacacaagtgtagtag 2523

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 351203 seqs, 113238999 residues

Total number of hits satisfying chosen parameters: 702406

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	132.8	5.3	1318	3	US-09-183-253-3
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6	39.2	1.6	248	4	US-09-244-796-32
7	39.2	1.6	277	4	US-09-007-005-3
8	39.2	1.6	277	4	US-09-244-796-3
9	35.8	1.4	748	1	US-08-361-467B-3
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12	35	1.4	3344	1	US-08-481-206-13
13	35	1.4	3344	2	US-08-486-269A-13
14	34.6	1.4	721	4	US-08-998-416-803
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c 16	34.6	1.4	2720	3	US-08-646-273-35
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18	33	1.3	4865	3	US-08-894-017-24
19	33	1.3	5177	6	5352450-1
c 20	32.8	1.3	12145	3	US-08-968-563-19
c 21	32.8	1.3	12145	3	US-08-969-683A-19
22	32.6	1.3	289	4	US-09-007-005-17
23	32.6	1.3	289	4	US-09-244-796-17
c 24	32.6	1.3	1703	3	US-08-646-273-18
c 25	32.6	1.3	1219	3	US-08-646-273-22
c 26	32.6	1.3	2314	3	US-08-646-273-29
c 27	32.6	1.3	2889	1	US-08-289-112-1

Query Match 6.4%; Score 162.2; DB 3; Length 2887;
Best Local Similarity 49.2%; Pred. No. 7.4e-42;

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29 32 1.3 30001 2 US-08-474-933-1 Sequence 1, Appli
c 30 31.8 1.3 802 4 US-08-896-164-12 Sequence 12, Appli
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33 31.6 1.3 1753 4 US-08-205-697A-6 Sequence 6, Appli
34 31.6 1.3 1753 4 US-08-702-525-6 Sequence 6, Appli
35 31.6 1.3 1753 5 PCT-US95-02576-6 Sequence 6, Appli
36 31.6 1.3 2149 1 US-08-784-651-3 Sequence 3, Appli
37 31.4 1.2 2333 1 US-08-427-993B-2 Sequence 2, Appli
38 31.4 1.2 2333 2 US-08-478-609A-2 Sequence 2, Appli
c 39 31.2 1.2 1605 4 US-09-124-541-3 Sequence 3, Appli
c 40 31.2 1.2 2730 3 US-08-936-135-17 Sequence 17, Appli
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c 42 31.2 1.2 3607 1 US-08-847-351B-1 Sequence 1, Appli
43 31.2 1.2 9997 1 US-08-246-982A-15 Sequence 15, Appli
44 31.2 1.2 9997 1 US-08-453-265-15 Sequence 15, Appli
45 31.2 1.2 10103 2 US-08-457-273B-7 Sequence 7, Appli

ALIGNMENTS

RESULT 1
US-09-183-253-1
; Sequence 1, Application US/09183253
; Patent No. 6043054
; GENERAL INFORMATION:
; APPLICANT: VAWTER, LISA
; APPLICANT: STAMMERS, MELANIE
; TITLE OF INVENTION: NOVEL COMPOUNDS
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Ratner & Prestia
; STREET: P.O. Box 980
; CITY: Valley Forge
; STATE: PA
; COUNTRY: USA
; ZIP: 19482
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09183,253
; FILING DATE: 30-OCT-1998
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 9817907.0
; FILING DATE: 17-AUG-1998
; APPLICATION NUMBER: 60/075,306
; FILING DATE: 20-FEB-1998
; ATTORNEY/AGENT INFORMATION:
; NAME: Prestia, Paul F
; REGISTRATION NUMBER: 23,031
; REFERENCE/DOCKET NUMBER: GP-70395
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 610-407-0700
; TELEFAX: 610-407-0700
; TELEX: 846169
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2887 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
US-09-183-253-1

Qy 2109 atcgcaacaggagcgccttggcccttcggtcttagctagctgatatctctgtgtttccot 2168
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

Db 1896 GGACCAGCCCAATGTGCAGTCTGTCATCGTGCTGGTCTGTCATCATCTTTGCAGCACCAT 1955

Qy 2169 aagcatgctgcgaatttgaccaaagtcat 2201
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

Db 1956 CACCCCTCTCCCGGTATTCTGCCGAAGCTCAT 1988

RESULT 2
US-09-183-253-3
; Sequence 3, Application US/09183253
; Patent No. 6043054
; GENERAL INFORMATION:
; APPLICANT: VAWTER, LISA
; APPLICANT: STAMMERS, MELANIE
; TITLE OF INVENTION: NOVEL COMPOUNDS
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Ratner & Prestia
; STREET: P.O. Box 980
; CITY: Valley Forge
; STATE: PA
; COUNTRY: USA
; ZIP: 19482
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/183,253
; FILING DATE: 30-OCT-1998
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 9817907.0
; FILING DATE: 17-AUG-1998
; APPLICATION NUMBER: 60/075,306
; FILING DATE: 20-FEB-1998
; ATTORNEY/AGENT INFORMATION:
; NAME: Prestia, Paul F
; REGISTRATION NUMBER: 23,031
; REFERENCE/DOCKET NUMBER: GP-70395
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 610-407-0700
; TELEFAX: 610-407-0700
; TELEX: 846169
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1318 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
US-09-183-253-3

	Query Match	5.3%;	Score 132.8;	DB 3;	Length 1318;
	Best Local Similarity	48.9%;	Pred. No. 1.4e-32;		
	Matches 511;	Conservative	0;	Mismatches 517;	Indels 18; Gaps 5;
QY	1038	cgccctacagtcagtggtgagtggtggtttggctttcaacaagaccatggaacgattg--	1095		
DB	243	CGCCCTACGATGTCATCTGGTTCATCGCCAAGACACTGCAGAGGGGCCATGGAGACACTGCA	302		
QY	1096	---acaacccgggaagaatctctgagggattttacctatacgacaaggagatlgcgca	1151		
DB	303	TGCCAGACCGCGCACCGGATTCAGGACTTCAACTACACGGACACACACCGCTGGGAG	362		
QY	1152	tgaatatctacgctgcgatgaactccacacaatttctgggtgtatcgggtgtggtggcatt	1211		
DB	363	GATCATCTCTCAATGCTCAACACGACACCAACTTCTTCGGGCTACGGGCTCAAGTGTATT	422		


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/ NAME/KEY: other
/ LOCATION: complement(223..295)
/ IDENTIFICATION METHOD: blastn
/ OTHER INFORMATION: identity 97
/ OTHER INFORMATION: region 1..73
/ OTHER INFORMATION: id AA038839
/ OTHER INFORMATION: est
/ FEATURE:
/ NAME/KEY: other
/ LOCATION: 326..387
/ IDENTIFICATION METHOD: blastn
/ OTHER INFORMATION: identity 91
/ OTHER INFORMATION: region 2..63
/ OTHER INFORMATION: id W51392
/ OTHER INFORMATION: est
/ FEATURE:
/ NAME/KEY: sig_peptide
/ LOCATION: 152..268
/ IDENTIFICATION METHOD: Von Heijne matrix
/ OTHER INFORMATION: score 5.9
/ OTHER INFORMATION: seq SVSLSLGIVLA/VV
/ US-08-905-223-216
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Query Match 3.1%; Score 79.2; DB 4; Length 397;
Best Local Similarity 50.9%; Pred. No. 1.4e-15;
Matches 201; Conservative 3; Mismatches 190; Indels 1; Gaps 1;

QY 1181 aattctgggtggtcgggtggtggcattcagttctcaggcgcatgtattgctctta 1240
Db 1 ACITTAGGGTCTCTGGCCATGTGGTGTGTGATGCCAGCBGCTCTCGATGGCATGA 60

QY 1241 cacagatcgaacgatgatagacgcaagtagcaggaagttgggttactacgatactcagt 1300
Db 61 CGCTTATCAGCAGCTTCAGGTGCGCAGCTACAAGAGATTGGCTACTATGACAGCACCA 120

QY 1301 tggataacctatctggttgtaactgaacagtgatggtggcagggttctctcaagatc 1360
Db 121 AGGATGATCTTCTGTCGTCACAAACAGATAAATGATTTGGAGGGTCCCCCAGCTGRSC 180

QY 1361 gcaaatgtcaccatgttctacgacccgtgtctctccattattgtgtcagtgtgca 1420
Db 181 AGACCTGGTGCATCAAGACATTCCTGCTGTCACAG-ANNNCCTTATCTCCGCTCAG 239

QY 1421 caatatcagttgtggcattctgtgcttcgcttgatcatctttaatatatgaata 1480
Db 240 TTCCTCCAGCCTGGGCATTGCTAGCTGTGTCTGTCTGTCCTTTAATCATCTACAAC 299

QY 1481 agcatagaagagtaatacaactcgcacatcccggtttgcaatacgcatactgtttgtg 1540
Db 300 CACATGTCCGTTATATCCAGAACTCACAGCCCAACCTGAACAACTGACTGTGTGGGCT 359

QY 1541 tcatactgtcctaatactatctcatcttaactgggc 1575
Db 360 GCTCMTGGCTTACGCTGCTGCTTCCCTCGGGC 394
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RESULT 4
US-08-232-463-14/C
; Sequence 14, Application US/08232463
; Patent No. 5670367
; GENERAL INFORMATION:
; APPLICANT: DORNER, F.
; APPLICANT: SCHEIFLINGER, F.
; APPLICANT: FALKNER, F. G.
; TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
; NUMBER OF SEQUENCES: 52
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 1800 Diagonal Road, Suite 500
; CITY: Alexandria
; STATE: VA
; COUNTRY: USA
```

```
/ ZIP: 22313-0299
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/232,463
/ FILING DATE:
/ CLASSIFICATION: 435
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US/07/935,313
/ FILING DATE:
/ APPLICATION NUMBER: EP 91 114 300.6
/ FILING DATE: 26-AUG-1991
/ ATTORNEY/AGENT INFORMATION:
/ NAME: BENT, Stephen A.
/ REGISTRATION NUMBER: 29,768
/ REFERENCE/DOCKET NUMBER: 30472/114 IMMU
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (703)836-9300
/ TELEFAX: (703)683-4109
/ TELEX: 899149
/ INFORMATION FOR SEQ ID NO: 14:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 7218 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ IMMEDIATE SOURCE:
/ CLONE: pTZ9pt-Fls
/ US-08-232-463-14
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Query Match 2.1%; Score 51.8; DB 1; Length 7218;
Best Local Similarity 6.3%; Pred. No. 7.6e-06;
Matches 26; Conservative 215; Mismatches 172; Indels 0; Gaps 0;

QY 791 ggtcagaggaactggtcagagtgatctgaagcagagggcagcgcacacacgtgtg 850
Db 1430 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1371

QY 851 aacagatgcgaatagtcgcgaagacatctgacacggaagcgcctcatgtggaatcaga 910
Db 1370 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1311

QY 911 acaatcagacaaactatccggaatgactgcagaggaatttcgacatcgactgaatcagg 970
Db 1310 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1251

QY 971 cgctaatcggagggtttagcacattaccacgacgcctatcccgaggagatcagagg 1030
Db 1250 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1191

QY 1031 cgccactcgcctacgagtgagtggtgagtggtgttggtttggtttcaacaagaccatggaac 1090
Db 1190 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1131

QY 1091 gattgacaacccgggaagaatactctgaggattttacctatacggacaagagattgccg 1150
Db 1130 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1071

QY 1151 atgaatctacgctgccatgaactccacaaatttctgggtgtgtatcggtgtgtg 1203
Db 1070 RRRATCGAAGCTCCCTCGACCTGCAGCCCAAGCTCGGAATTAATTCTGTGAG 1018
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```
RESULT 5
US-09-007-005-32
; Sequence 32, Application US/09007005B
; Patent No. 6258558
; GENERAL INFORMATION:
; APPLICANT: Szostak, Jack W.
```

```

; APPLICANT: Roberts, Richard W.
;
; APPLICANT: Liu, Rine
;
; TITLE OF INVENTION: SELECTION OF PROTEINS USING RNA-PROTEIN
;
; TITLE OF INVENTION: FUSIONS
;
; FILE REFERENCE: 00786/350003
;
; CURRENT APPLICATION NUMBER: US/09/007.005B
;
; CURRENT FILING DATE: 1998-01-14
;
; EARLIER APPLICATION NUMBER: 60/035.963
;
; EARLIER FILING DATE: 1997-01-27
;
; EARLIER APPLICATION NUMBER: 60/064.491
;
; EARLIER FILING DATE: 1997-11-06
;
; NUMBER OF SEQ ID NOS: 33
;
; SOFTWARE: FastSEQ for Windows Version 4.0
;
; SEQ ID NO 32
;
; LENGTH: 248
;
; TYPE: RNA
;
; ORGANISM: Homo sapiens
;
; US-09-007-005-32

```

Query Match	1.6%	Score 39.2;	DB 4;	Length 248;
Best Local Similarity	16.4%;	Pred. No. 0.0087;		
Matches 39;	Conservative 95;	Mismatches 104;	Indels 0;	Gaps 0;
QY	749	agcagctatagccgagctcatgtgtgtcttattgctgtgctacgagacaactggt	808	
		l:l: : : : : l: : : : : : : : : : : l:l: : : : : l:l: : : : : l:l: : : : :		
Db	8	arcararururcrururururcrararururcrararurgrcrgurgrar	57	
QY	809	acgaggtgaaatctgaacgagcagggcatacctgcactgttgacagatgcgaatagctg	868	
		l: : : : : l:l: : : : l: : : : : l: : : : : l: : : : : l: : : : : l: : : : :		
Db	68	argrararcrgrarararcrurgrarurcrurgrarargrargrarcrur	127	
QY	869	cgcgaagcactctgacaacgcgaagcgctcatgttggaatccagaacaactat	928	
		l:l: : : : : l: : : : : l: : : : : l: : : : : l: : : : : l: : : : : l: : : : :		
Db	128	grcrgcrgururarararcrgrurgrurgrararcrarcrgrarararcrar	187	
QY	929	ccggaatgactgcagaggaatttcgacatcgactgaatcaggcgctaactcaggagg	986	
		l: : : : : l: : : : : l: : : : : l: : : : : l: : : : : l: : : : : l: : : : :		
Db	188	crararcrgrgrararararcrgrarcrgrurararcrurcrurgrcr	245	

```

RESULT 6
US-09-244-796-32
; Sequence 32, Application US/09244796
; Patent No. 6281344
; GENERAL INFORMATION:
; APPLICANT: Szostak, Jack W.
; APPLICANT: Roberts, Richard W.
; APPLICANT: Liu, Rihe
; TITLE OF INVENTION: SELECTION OF PROTEINS USING RNA-PROTEIN
; TITLE OF INVENTION: FUSIONS
; FILE REFERENCE: 00786/350007
; CURRENT APPLICATION NUMBER: US/09/244,796
; CURRENT FILING DATE: 1999-02-05
; EARLIER APPLICATION NUMBER: 60/035,963
; EARLIER FILING DATE: 1997-01-27
; EARLIER APPLICATION NUMBER: 60/064,491
; EARLIER FILING DATE: 1997-11-06
; EARLIER APPLICATION NUMBER: 09/007,005
; EARLIER FILING DATE: 1998-01-14
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 32
; LENGTH: 248
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-244-796-32

```

```
Query Match      1.6%; Score 39.2; DB 4; Length 248;
Best Local Similarity 16.4%; Pred. NO. 0.0087;
Matches 39; Conservative 95; Mismatches 104; Indels 0; Gaps 0;
```

```

Qy 749 agcagctatagccagactcatgtgtgttctttattggctgtgtacagagacaactggt 808
| : : : : : | : : : : : : : : : : : : : : : : : : : : : : : : :
Db 8 arcraarururururururururururururururururururururgrcgrurgr 67
| : : : : : | : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 809 acgaagtgaattgaaacagagggcatcacctgcactgttgaaacagatgcgaatagctg 868
| : : : : : | : : : : : : : : : : : : : : : : : : : : : : : : :
Db 68 argarararargrararararurururururururururururururururgrarcr 127
| : : : : : | : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 869 ccgaaggacatctgacaacgaagcgctcatgtggaatcagaacaatcagacaactat 928
| : : : : : | : : : : : : : : : : : : : : : : : : : : : : : : :
Db 128 gcrurgrcgrurarararururururururururururururururururgrararcr 187
| : : : : : | : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 929 ccggaatgactgcagaggaatttcagacatgcactgaatcaggcgctaatcagagagg 986
| : : : : : | : : : : : : : : : : : : : : : : : : : : : : : : :
Db 188 crararcrurgrararararargrcgrcgrurururururururururgrcgr 245

RESULT 7
US-09-007-005-3
; Sequence 3, Application US/09007005B
; Patent NO. 6258558
; GENERAL INFORMATION:
; APPLICANT: Szostak, Jack W.
; APPLICANT: Roberts, Richard W.
; APPLICANT: Liu, Rihe
; TITLE OF INVENTION: SELECTION OF PROTEINS USING RNA-PROTEIN
; FILE REFERENCE: 00786/350003
; CURRENT APPLICATION NUMBER: US/09/007.005B
; CURRENT FILING DATE: 1998-01-14
; EARLIER APPLICATION NUMBER: 60/035,963
; EARLIER FILING DATE: 1997-01-27
; EARLIER APPLICATION NUMBER: 60/064,491
; EARLIER FILING DATE: 1997-11-06
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 277
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Translation template
US-09-007-005-3

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[illegible]

RESULT 8
US-09-244-796-3
; Sequence 3, Application US/09244796
; Patent No. 6281344
; GENERAL INFORMATION:
; APPLICANT: Szostak, Jack W.
; APPLICANT: Roberts, Richard W.

RESULT 11
US-07-718-575-13
; Sequence 13, Application US/07718575
; Patent No. 5202257
; GENERAL INFORMATION:
; APPLICANT: Heinemann Ph.D., Stephen F.
; APPLICANT: Boulter Ph.D., James R.
; APPLICANT: Hollmann Ph.D., Michael NNN

Qy	36	gtttggaatttttcttgatttaacgcctcgccagcactgcaaggggcgctggccgg	95
Dy	37		
Db	39	GGTTTGGGAATACTGGCCCGGTTCTTCGTGCCTTGATCCAGACTCGCGCGG	98
Qy	96	gagcccgatgaacctgcacatcgcatcgcgacaaccttcgatagcgcgaaaggagatggca	155
Dy	97		
Db	99	GATGCCCACGTATCATCGGATCGCGGAATCTTTGAGTAGCGCGACGGCCCCAACGCCCA	158
Qy	156	ggcgccgacggctgtatgcctgccacaagaactggcgttgtatgtccaacagcagcc	215
Dy	157		
Db	159	GGTCATGAAGCCTGAGGAGCAGCGCTTTTCGGTATTTCGCCAATATCATCAACAGGAACAG	218
Qy	216	gaatctgctccgggctctaagtctaccctgcacagcaacagcagcgagtgtgagccgg	275
Dy	217		
Db	219	AACTCTGCTGCCCMACAGACCCTTGACCTACGACATTCAGAGGATTCCTCCATGACAG	278
Qy	276	tttggcgccagcgtgatg	294
Dy	277		
Db	279	TTTTTAGGCCCAACAAGAAG	297

```
RESULT 12
US-08-481-206-13
; Sequence 13, Application US/08481206
; Patent No. 5739291
; GENERAL INFORMATION:
; APPLICANT: Heinemann Ph.D., Stephen F.
; APPLICANT: Boulter Ph.D., James R.
; APPLICANT: Hollmann Ph.D., Michael NMN
; APPLICANT: Bettler Ph.D., Bernhard NMN
; APPLICANT: Jensen Ph.D., Jan E.
; TITLE OF INVENTION: GLUTAMATE RECEPTOR COMPOSITIONS AND
; METHODS
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pretty, Schroeder, Brueggemann & Clark
; STREET: 444 So. Flower St., Suite 2000
; CITY: Los Angeles
; STATE: California
; COUNTRY: United States
; ZIP: 90071-2921
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/481,206
; FILING DATE:
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/013,767
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Reiter Ph.D., Stephen E.
; REGISTRATION NUMBER: 31192
; REFERENCE/DOCKET NUMBER: P31 8962
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; TELEX: 9103330318
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3344 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; ORIGINAL SOURCE:
; CELL TYPE:
; CELL LINE:
; IMMEDIATE SOURCE:
; LIBRARY:
; CLONE: Glur7
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..2766
US-08-481-206-13

Query Match 1.4%; Score 35; DB 1; Length 3344;
Best Local Similarity 45.9%; Pred. No. 1.2;
Matches 119; Conservative 0; Mismatches 140; Indels 0; Gaps 0;

QY 36 gttttgatatatttgcctgtttgttttaacgtcctcgccgacacgtgcaagggcggtgcccgg 95
DB 39 GGTGTTGGGAATACTGGCGCGGGTTCGTCGTGTCGCCCTTCGGATCCACAGACTCGCGCGG 98
QY 96 gagggccgatgaactgcacatcgccgcatctttccgatagccgcaaaaggaggatggca 155
DB 99 GATGCCCCAGTCATCCGGATCGCGGAATCTTTGATACGCGGACGGCCCAACGCCCA 158
QY 156 gggcgccagcggtgtatgctgctgccacaagactggtggtgatgtgtcaacaagagcc 215
|||||
|||||

Db 159 GGTCAAGAACGCTGAGGAGCACCCTTTTCGGTTTTCTGCCAATATCATCAACAGGACAG 218
QY 216 gaatctgtccggggcttcaagctcatctgcacagcagcagcagcagcagcagcagcagc 275
|||||
Db 219 AACTCTGCTGCCCAACACGACGCTGACCTACGACATTTCAGAGGATTCACTTCCATGACAG 278
QY 276 tttgggcccagcagcgtgatg 294
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Db 279 TTTTGAGGCCACCACGAAG 297
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RESULT 13
US-08-486-269A-13
; Sequence 13, Application US/08486269A
; Patent No. 5945509
; GENERAL INFORMATION:
; APPLICANT: Heinemann, Stephen F.
; APPLICANT: Boulter, James R.
; APPLICANT: Hollmann, Michael
; APPLICANT: Bettler, Bernhard
; APPLICANT: Jensen, Jan E.
; TITLE OF INVENTION: GLUTAMATE RECEPTOR COMPOSITIONS
; AND METHODS
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Gray Cary Ware & Freidenrich LLP
; STREET: 4365 Executive Drive, Suite 1600
; CITY: San Diego
; STATE: CA
; COUNTRY: USA
; ZIP: 92121
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows DEMONSTRATION Version 2.0D
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/486,269A
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/013,767
; FILING DATE: 04-FEB-1993
; APPLICATION NUMBER: 07/718,575
; FILING DATE: 21-JUN-1991
; APPLICATION NUMBER: PCT/US90/06153
; FILING DATE: 25-OCT-1990
; APPLICATION NUMBER: 07/428,116
; FILING DATE: 27-OCT-1989
; ATTORNEY/AGENT INFORMATION:
; NAME: Reiter, Stephen E.
; REGISTRATION NUMBER: 31,192
; REFERENCE/DOCKET NUMBER: P41 9986
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-677-1409
; TELEFAX: 619-677-1465
; TELEX:
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3344 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; IMMEDIATE SOURCE:
; CLONE: Glur7
; FEATURE:
; NAME/KEY: Coding Sequence
; LOCATION: 1...2763
; OTHER INFORMATION:
US-08-486-269A-13
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	Query Match	1.4%	Score 34.6;	DB 4;	Length 721;	
	Best Local Similarity	53.3%;	Pred. No.	0.56;		
	Matches	73;	Conservative	0;	Mismatches	64; Indels 0; Gaps 0;
QY	357	caccacgtgagcggctgcacaaatgtgaataattgctctgtctaaggccctc	416			
Db	341	CTCTTGTGTAAGATGTTGGCCGTCTGTGAACCGACTGTGCCCTCGGTGTGGC	400			
QY	417	gagtcgggctcttccgatcgcaaacgactcccacctattccgcacccatccatgcc	476			
Db	401	GAGCGAGTCTGTCGACGACGCAGNATCTTGCTATACACCCACACACCCTCGAATGT	460			
QY	477	cacgggtgcacaatccaa	493			
Db	461	ACGGATGCAACAGTCAA	477			

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, COUNTRY: USA
, ZIP: 20036
, COMPUTER READABLE FORM:
, MEDIUM TYPE: Diskette, 3.5 inch, 1.4 Mb storage
, COMPUTER: IBM AT-compatible, 80486 processor
, OPERATING SYSTEM: MS-DOS version 6.0
, SOFTWARE: WordPerfect version 5.1
, CURRENT APPLICATION DATA:
, APPLICATION NUMBER: US/08/646,273
, FILING DATE: 16-NOV-1994
, CLASSIFICATION: 435
, PRIOR APPLICATION DATA:
, APPLICATION NUMBER: PCT/EP94/03706
, FILING DATE: 11-NOV-1994
, INFORMATION FOR SEQ ID NO: 24:
, SEQUENCE CHARACTERISTICS:
, LENGTH: 2533 base pairs
, TYPE: nucleic acid
, STRANDEDNESS: single
, TOPOLOGY: linear
, MOLECULE TYPE: cDNA for mRNA
, US-08-646-273-24

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	Query Match Best Local Similarity Matches	1.4%; 51.6%; 79;	Score 34.6; Pred. No. 1.4; Conservative	DB 3; Mismatches 74;	Length 2533; Indels 0;	Gaps 0;
QY	635	tctatccgatccaacagacgcgcgtgcgcgaatttgcagcccgaggatgcacgcatacttg	694			
Db	1520	TTCTTGTGGCGGAGTAGTAGCGCTTCACCATGGCGGGGTGATGCTCCATGATCTCTG	1461			
QY	695	tgggaactctctatgtagtgagcgcgcagaggagggtgctctgcgaaatgtacaaacacgagc	754			
Db	1460	TTGGGGGCGCTTCCCTTGAGCTGATCGGCGAGTAGACCCCTCCATGAGAAGTTGAAAAACCGCATG	1401			
QY	755	tatatgcccagacgtccatgtagtgcattctatttg	787			

Db 1400 GCATTTCAAGTAGAGGCTGTGGAACCTGCACTG 1368
| | | | | | | | | | | | | | | | | |

Search completed: May 1, 2002, 04:25:03
Job time: 9363 sec

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: May 1, 2002, 02:48:15 ; Search time 231.77 Seconds
(without alignments)
9332.664 Million cell updates/sec

Title: US-09-715-962-1
Perfect score: 2523
Sequence: 1 atgcgcaagatgacaag.....caatcacacaagtgagtag 2523

Scoring table:

IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 930621 seqs, 428662619 residues

Total number of hits satisfying chosen parameters: 1861242

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

N_Geneseq_1101:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2523	100.0	2523	22	AAH20519
2	571.4	22.6	2895	20	AAH20519
3	570.6	22.6	2886	22	AAH20519
4	569.4	22.6	2535	20	AAH20519
5	569.4	22.6	2602	20	AAH20519
6	569.4	22.6	2620	19	AAH20519
7	569.4	22.6	2679	20	AAH20519
8	569.4	22.6	2700	20	AAH20519
9	569.4	22.6	2822	21	AAH20519
10	569.4	22.6	2886	20	AAH20519
11	569.4	22.6	2886	20	AAH20519

12	569.4	22.6	2887	20	AAH20519	Human GABABR1b rec
13	569.4	22.6	2914	21	AAH20519	Human GABABR1a rec
14	569.4	22.6	2924	19	AAH20519	Human GABA-BR1b re
15	569.4	22.6	3464	20	AAH20519	Human GABABR1a cod
16	569.4	22.6	3464	20	AAH20519	Human GABABR1a cod
17	569.4	22.6	3969	20	AAH20519	GABA-BR1a*Gqo5 fus
18	569.4	22.6	4565	22	AAH20519	Human brain cell s
19	566.8	22.5	4220	20	AAH20519	Human GABA B recep
20	563.6	22.3	4220	22	AAH20519	Human GABA-B-R1a c
21	558	22.1	2883	20	AAH20519	Murine gamma-amino
22	558	22.1	2883	22	AAH20519	Murine GABA-B-R1a
23	554.8	22.0	2532	20	AAH20519	Rat GABABR1b codin
24	554.8	22.0	2837	19	AAH20519	Rat GABA-BR1b rece
25	554.8	22.0	2880	20	AAH20519	Rat GABABR1a codin
26	554.8	22.0	4376	19	AAH20519	Rat GABA-BR1a rece
27	553	21.9	2661	20	AAH20519	Human GABAB recep
28	523.8	20.8	2518	20	AAH20519	Human GABAB recep
29	520.8	20.6	3127	20	AAH20519	Human GABABR1b cod
30	392	15.5	1746	20	AAH20519	Canine GABAB recep
31	374.4	14.8	1386	20	AAH20519	Human GABAB recep
32	374.4	14.8	1737	20	AAH20519	Human GABAB recep
33	338.2	13.4	2367	20	AAH20519	Human GABAB recep
34	337.8	13.4	2489	20	AAH20519	Human GABAB recep
35	271.4	10.8	1692	20	AAH20519	Human GABAB recep
36	222.4	8.8	5459	21	AAH20519	Rat gb2 GABA B rec
37	220.2	8.7	2823	21	AAH20519	Rat gamma amino bu
38	219.2	8.7	3288	21	AAH20519	Rat GABA-B recepto
39	219.2	8.7	3288	21	AAH20519	Rat GABA-B recepto
40	218.6	8.7	2652	20	AAH20519	Rat GABA-B recepto
41	211.6	8.4	3256	21	AAH20519	CDNA encoding a hu
42	210	8.3	2823	20	AAH20519	Human partial GABA
43	210	8.3	2826	21	AAH20519	Human GABA-B recep
44	210	8.3	2826	21	AAH20519	Human GABA-B recep
45	210	8.3	2826	21	AAH20519	Human GABA-B-R2 re

ALIGNMENTS

RESULT 1
AAH20519
ID AAH20519 standard; DNA; 2523 BP.
XX
AC AAH20519;
XX
DT 03-AUG-2001 (first entry)
XX
DE D. melanogaster GABA-B receptor DNA SEQ ID 1.
XX
KW GABA-B receptor; fruitfly; gamma-aminobutyric acid B receptor;
KW insecticide; transgenic invertebrate; plant protection agent;
KW human medicine; veterinary medicine; insect; ds.
XX
OS Drosophila melanogaster.
XX
PN DE19955408-A1.
XX
PD 23-MAY-2001.
XX
PF 18-NOV-1999; 99DE-1055408.
XX
PR 18-NOV-1999; 99DE-1055408.
XX
PA (FARB) BAYER AG.
XX
PI Raming K, Mezler M, Mueller T;
XX
DR WPI: 2001-318282/34.
DR P-PSDB; AAB86159.
XX
PT New invertebrate gamma-aminobutyric acid receptor proteins, useful in
PT screening for potential insecticides, for plant protection or medicine,
PT also related nucleic acid

XX	Claim 6; Page 8-15; 62pp; German.	
PS	This invention describes a novel polypeptide (I), functioning as a	
CC	gamma-aminobutyric acid -B (GABA-B) receptor which has insecticidal	
CC	activity. (I), also the nucleic acid (II) that encodes it and related	
CC	vectors, host cells, antibodies and transgenic invertebrates, are used	
CC	for identifying: (i) new plant protection agents, i.e. modulators of (I)	
CC	with insecticidal activity, which may also be useful in human or	
CC	veterinary medicine; and (ii) genes that encode polypeptides involved in	
CC	assembly of functionally related GABA-B receptors in insects. This	
CC	sequence encodes a fruitfly (Drosophila melanogaster) GABA-B receptor	
XX	which is described in the method of the invention.	
SQ	Sequence 2523 BP; 650 A; 605 C; 653 G; 615 T; 0 other;	
	Query Match 100.0%; Score 2523; DB 22; Length 2523;	
	Best Local Similarity 100.0%; Pred. No. 0;	
	Matches 2523; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
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RESULT 2
AAX58058
ID AAX58058 standard; cDNA to mRNA; 2895 BP.
AC AAX58058;
XX AAX58058;
XX AAX58058;
DT 21-JUL-1999 (first entry)
XX 21-JUL-1999 (first entry)
DE Canine GABAB receptor 1a coding sequence.
DE Canine GABAB receptor 1a coding sequence.
KW GABAB receptor; gamma aminobutyric acid type B receptor; inhibitor;
KW transient lower oesophageal sphincter relaxation; spasticity; emesis;
KW gastro-oesophageal reflux disease; epilepsy; psychiatric disorder; TLESR;
KW irritable bowel syndrome; dyspepsia; arthritis; allergy; diagnosis;
KW autoimmune disease; neoplastic disease; infectious disease; therapy; ss.
XX Canis familiaris.
OS Canis familiaris.
XX WO9921890-A1.
XX PD 06-MAY-1999.
XX PF 27-OCT-1998; 98WO-SE01947.
XX PR 17-JUL-1998; 98SE-0002575.

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PR 27-OCT-1997; 97SE-0003914.
XX 16-MAR-1998; 98SE-0000864.
PA (ASTR ) ASTRA AB.
XX Ekstrand J;
XX WPI: 1999-302985/25.
XX P-PSDB; AAY14105.
PT Polynucleotides encoding human and canine gamma aminobutyric acid
PT type B receptors, used to screen for compounds that are inhibitors
PT of transient lower oesophageal sphincter relaxations
XX Claim 13; Page 99-105; 222pp; English.
XX This sequence encodes a canine gamma aminobutyric acid type B (GABAB)
CC receptor of the invention. Nucleic acid molecules encoding GABAB
CC receptors can be used to screen for compounds that are inhibitors of
CC transient lower oesophageal sphincter relaxations (TLESR). They can also
CC be used to screen for agonists or antagonists of the GABAB receptors.
CC Inhibitors of TLESR are useful for treating gastro-oesophageal reflux
CC disease. Other uses of GABAB receptors, such as human GABAB R1c or 1d,
CC comprise diagnosis or treatment of conditions related to GABAB
CC dysfunction, e.g. epilepsy, psychiatric disorders, emesis, irritable
CC bowel syndrome, dyspepsia, spasticity, arthritis, allergies, autoimmune
CC diseases, neoplastic diseases, pain and infectious disease.
XX Sequence 2895 BP; 610 A; 835 C; 842 G; 608 T; 0 other;
SQ

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Query Match 22.6%; Score 571.4; DB 20; Length 2895;
Best Local Similarity 55.0%; Pred. No. 1e-170;
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Db 2305 atgaacacctggtctggcattttctatggttacaagggtgctgtctgtctgtaggcac 2364
QY 1984 ttttggctacgagcgcgctcca ttaagtgaacagatcaacagattcgcggttatctgt 2043
Db 2365 tttctgtctatgagaccaagcgtgtctactgagaagatcaatgaccacccgggtgtg 2424
QY 2044 ggcagagcatctatacgtgtgtccttgccttgctgataaacagctccggtggcagtgctc 2103
Db 2425 ggcattggccatgtacaacgtggcgttctgtctcactcactgccccggctccatgac 2484
QY 2104 attgcatcgcaacagcgcgtcttgccttgcctgtgtctgtctgtatcttctgtgt 2163
Db 2485 ctgtccagcagcagatgcagcttgccttgcagctcttgcctatgctgtctctctcc 2544
QY 2164 ttctcaagcatgctgtctgatatgttggccaaaggctattgaggttatcagctcatcccaag 2223
Db 2545 tacatcactctgtgtctgtctgtctgtgcggaagatgcgcaggttgatcacccgggttgag 2604
QY 2224 gataaggcgaatcgaaaaatacaatccgattccagccatatcgaaaaggagcagaagaacgc 2283
Db 2605 tggcagtcggagggcgagataccatgaaacgggtgctgcaccaacaacatgaggaa 2664
QY 2284 tatcagaactgtttaccgaaaaacgagcaattgcaacgattacaacagagaggagaa 2343
Db 2665 gagaagctccgactgttgagaaggagaccgggagctggagagatcattgtgtgaaa 2724
QY 2344 aagattcagat 2354
Db 2725 gaggaagcagat 2735

RESULT 3

AAC91925

ID AAC91925 standard; cDNA; 2886 BP.

AC AAC91925;

XX

DT 19-MAR-2001 (first entry)

XX Human GABA-B-R1a coding sequence #1.

XX Human; gamma-amino-butyric acid receptor; GABA-B; ss.

XX Homo sapiens.

XX WO200073788-A1.

XX 07-DEC-2000.

XX 30-MAY-2000; 2000WO-CA00638.

XX 01-JUN-1999; 99US-0137025.

XX (MERI) MERCK FROSST CANADA & CO.

XX Ng G, O'Neill G;

XX WPI: 2001-049959/06.

XX P-PSDB; AAB50090.

XX Use of gabapentin, 1-(aminomethyl)cyclohexanecarboxylic acid, in assays for
PT identifying gamma-amino-butyric acid (GABA)-B agonists and antagonists

ST
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XX 33

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The present invention relates to a method for determining whether a substance binds to gamma-amino-butyric acid (GABA)-B receptors and is a potential agonist or antagonist of the GABA-B receptor. The method comprises exposing cells to 1-(aminomethyl)cyclohexanecetic acid (gabapentin) in the presence or absence of the substance under investigation. The present sequence is a coding sequence for human GABA-B-R1a, which was used in the present invention to construct a functional GABA-B receptor, for use in the method of the present invention.

Sequence 2886 BP; 632 A; 822 C; 797 G; 634 T; 1 other;

Query Match 22.68; Score 570.6; DB 22; Length 2886;

Best Local Similarity 54.8%; Pred. No. 1.8e-170;

Matches 1231; Conservative 1; Mismatches 980; Indels 33; Gaps 4;

Qy 130 ccgatagccggcacaaggaggatggcaggggcggccaggcggtatgcctgcccacaaactg 189

DB 323 CTGTTTCCCATGAGCGGGGGCTGGCCAGGGGGGCCAGCCTGCCAGCCCGCGGTGGAGATG 582

Qy 190 gcgttgatgtcaacaagcagccgaatctgctgccgggttcaagctcatcctgcac 249

583

042

Qy 250 agcaacgacgagtgtagcccggttgggcgccagcgtgatgtacaatctgctctat 309

643 caccacgacacacaaattatccaggccaaaccacccaaat accctatataaacctactctac 702

22 23 24 25 26 27 28 29 30 31 32 33 34 35 36 37 38 39 40 41 42 43 44 45 46 47 48 49 50 51 52 53 54 55 56 57 58 59 60 61 62 63 64 65 66 67 68 69 70 71 72 73 74 75 76 77 78 79 80 81 82 83 84 85 86 87 88 89 90 91 92 93 94 95 96 97 98 99 100 101 102 103 104 105 106 107 108 109 110 111 112 113 114 115 116 117 118 119 120 121 122 123 124 125 126 127 128 129 130 131 132 133 134 135 136 137 138 139 140 141 142 143 144 145 146 147 148 149 150 151 152 153 154 155 156 157 158 159 160 161 162 163 164 165 166 167 168 169 170 171 172 173 174 175 176 177 178 179 180 181 182 183 184 185 186 187 188 189 190 191 192 193 194 195 196 197 198 199 200 201 202 203 204 205 206 207 208 209 210 211 212 213 214 215 216 217 218 219 220 221 222 223 224 225 226 227 228 229 230 231 232 233 234 235 236 237 238 239 240 241 242 243 244 245 246 247 248 249 250 251 252 253 254 255 256 257 258 259 260 261 262 263 264 265 266 267 268 269 270 271 272 273 274 275 276 277 278 279 280 281 282 283 284 285 286 287 288 289 290 291 292 293 294 295 296 297 298 299 300 301 302 303 304 305 306 307 308 309 310 311 312 313 314 315 316 317 318 319 320 321 322 323 324 325 326 327 328 329 330 331 332 333 334 335 336 337 338 339 340 341 342 343 344 345 346 347 348 349 350 351 352 353 354 355 356 357 358 359 360 361 362 363 364 365 366 367 368 369 370 371 372 373 374 375 376 377 378 379 380 381 382 383 384 385 386 387 388 389 390 391 392 393 394 395 396 397 398 399 400 401 402 403 404 405 406 407 408 409 410 411 412 413 414 415 416 417 418 419 420 421 422 423 424 425 426 427 428 429 430 431 432 433 434 435 436 437 438 439 440 441 442 443 444 445 446 447 448 449 450 451 452 453 454 455 456 457 458 459 460 461 462 463 464 465 466 467 468 469 470 471 472 473 474 475 476 477 478 479 480 481 482 483 484 485 486 487 488 489 490 491 492 493 494 495 496 497 498 499 500 501 502 503 504 505 506 507 508 509 510 511 512 513 514 515 516 517 518 519 520 521 522 523 524 525 526 527 528 529 530 531 532 533 534 535 536 537 538 539 540 541 542 543 544 545 546 547 548 549 550 551 552 553 554 555 556 557 558 559 560 561 562 563 564 565 566 567 568 569 570 571 572 573 574 575 576 577 578 579 580 581 582 583 584 585 586 587 588 589 590 591 592 593 594 595 596 597 598 599 600 601 602 603 604 605 606 607 608 609 610 611 612 613 614 615 616 617 618 619 620 621 622 623 624 625 626 627 628 629 630 631 632 633 634 635 636 637 638 639 640 641 642 643 644 645 646 647 648 649 650 651 652 653 654 655 656 657 658 659 660 661 662 663 664 665 666 667 668 669 670 671 672 673 674 675 676 677 678 679 680 681 682 683 684 685 686 687 688 689 690 691 692 693 694 695 696 697 698 699 700 701 702 703 704 705 706 707 708 709 710 711 712 713 714 715 716 717 718 719 720 721 722 723 724 725 726 727 728 729 730 731 732 733 734 735 736 737 738 739 740 741 742 743 744 745 746 747 748 749 750 751 752 753 754 755 756 757 758 759 760 761 762 763 764 765 766 767 768 769 770 771 772 773 774 775 776 777 778 779 780 781 782 783 784 785 786 787 788 789 790 791 792 793 794 795 796 797 798 799 800 801 802 803 804 805 806 807 808 809 810 811 812 813 814 815 816 817 818 819 820 821 822 823 824 825 826 827 828 829 830 831 832 833 834 835 836 837 838 839 840 841 842 843 844 845 846 847 848 849 850 851 852 853 854 855 856 857 858 859 860 861 862 863 864 865 866 867 868 869 870 871 872 873 874 875 876 877 878 879 880 881 882 883 884 885 886 887 888 889 890 891 892 893 894 895 896 897 898 899 900 901 902 903 904 905 906 907 908 909 910 911 912 913 914 915 916 917 918 919 920 921 922 923 924 925 926 927 928 929 930 931 932 933 934 935 936 937 938 939 940 941 942 943 944 945 946 947 948 949 950 951 952 953 954 955 956 957 958 959 960 961 962 963 964 965 966 967 968 969 970 971 972 973 974 975 976 977 978 979 980 981 982 983 984 985 986 987 988 989 990 991 992 993 994 995 996 997 998 999 1000 1001 1002 1003 1004 1005 1006 1007 1008 1009 1010 1011 1012 1013 1014 1015 1016 1017 1018 1019 1020 1021 1022 1023 1024 1025 1026 1027 1028 1029 1030 1031 1032 1033 1034 1035 1036 1037 1038 1039 1040 1041 1042 1043 1044 1045 1046 1047 1048 1049 1050 1051

Qy 310 aataaacgcaaaagctgatgctgttggcaggatgcagcacggtctgcaccactgtagcc 369

Db 703 aacqaccctatcaagatcatccttatgcctgagctgcagctctgtctccacgctggtgct 762

.....

Qy 370 gaggcgccaaaatgttggaatctaattgtgctctgtctaaggggcctcgagtcggctctt 429

Db 763 gaggtgctaggatgtggaacctcattgtgctttcctatggctccagctcaccagccctg 822

100

QY 430 TCGGATCGCAACGATTCGCCACTCTATCCGCCCATCCCATCGGCCACGCTGCACAAT 489

Db 823 tcaaacggcagcgtttcccacttttccgaaagcaccatcagccactccaac 882

[illegible][illegible]

Db 883 cctaccgcgtgaaactctttgaaaagtggggctggaagaagattgctaccatccagcag 942

Ov 550 qcgaggagggtcttttatatcgaccatagaggatctcgacaaatcgatatcatcgaagctgac 609

[illegible]

Db 943 accactgagggtcttcactctcgactctggacgacctggaggacgagtgaaggaggctgga 1002

Qy 610 qttqaaatcqttaactagacaatcatttctatccqatccaaacagacqccqatcgcgaattg 669

[illegible]

D6 1003 attgagattactttccgcagagtttcttctcagatccagctgtgccggtcaaaaacctg 106


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Db 1006 cgactgaaagacaccctcgaggaga-----caggaggcttccaggag 1047
Qy 1030 gcgcactcgctcagatcgagtgagtgagtggtgttggctttccaaacaaagaccatggaa 1089
Db 1048 gcacgctggcctatgcatcgatcgcttggccttggcactggccctgaaacaagacatctgga 1107
Qy 1090 cgattgacaaccgggaagaatctctgaggatatttacctatcacggaacaagagattgcc 1149
Db 1108 ggaggcgccgttctgtgtgctgaggaacttcaactacaacaacagaccattacc 1167
Qy 1150 gatgaatctacgctgccatgaactccacaaattctcgggtgtatcggtgtgtgtgga 1209
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Db 1228 ttgatccagcgctctcggtggtgcatgagcgttatacgagcagcttcaagggtggcagc 1287
Qy 1270 tacgagaagtgggttactacgatactcagttcagttgataacctatctcgttgaatactgaa 1329
Db 1288 tacaagaagattggtctactatgacagcaccagagatgatcttctcgttccaaacagat 1347
Qy 1330 cagtggttggtggcaagggttctcacaagtcgcacaattgtcaaccatgttctacgcacc 1389
Db 1348 aatggtattggagggtcccccacgctgacagaccctggctcaacaagacatccgccttc 1407
Qy 1390 gtgtccttgccattattgtgtgcatgtgcacaatatccagttgtggcatattctgtgcc 1449
Db 1408 ctgtcacagaactcttatctcgtctcagttctctcagcctgggcattgtctcagct 1467
Qy 1450 ttgccttgatcatctttaaataatataatggaataagacatagaagatgaatacaatccctcgat 1509
Db 1468 gttgtctgtctctttaaactataactacacatgcacatgccgttataccagaactcacag 1527
Qy 1510 cccgtttgcaatcagatcatgtatttgggtgtcatcatctgtcctaataatctgtctatcta 1569
Db 1528 cccaactgacaacctgactgctgtgtgggtgtcactggtctttagtctgtgcttcccc 1587
Qy 1570 ctgggcatcgacgagcgttctgtcagcccgaggagaataatccaaagatatgtcaagcggg 1629
Db 1588 ctggggctcgatggttaccacatgggaggaaccaggttctcttctgtctgccaggccgc 1647
Qy 1630 gcttggtactatccacggttttacacatgatacagtgctatgttccagcaagctctgg 1689
Db 1648 ctctggctctcggcctgggtttagtctgggtcaggttccatgttccaccaagatttgg 1707
Qy 1690 cgtgtgcatcgttttacaaca-----aagcaaaaactgaccccaaaaagaaagtga 1743
Db 1708 tgggtccacacggtcttcacaagaagaaagaaagagggagtgaggagactctggaa 1767
Qy 1744 ccttggagctatcacaccatggttctcgggctattataatagatttagtgatatattc 1803
Db 1768 ccttggagctgtatgccacagtggtcgtcgtgtggcagtgatgtctcactctcgc 1827
Qy 1804 tcatggcagatctttagtcgctcagcgttatctcgaacacattccccactcgaagatcca 1863
Db 1828 atctggcagatcgtggaccctctgaccggaccatttgagacatttgcgaaggagaaacct 1887
Qy 1864 gtatctactactgatataataaataacgtccagacttgagcattgtgaaagtcaacgc 1923
Db 1888 aaggaagatattgacg---tctctatctcgccacgctggagcattgcagctccagggaag 1944
Qy 1924 aactcctatggttgggtctgtatagcgttccaggggtcaatcctgtgttttggcctc 1983
Db 1945 atgaatacaggttggttctatgtgttacaagggtcgtgctgtctgtctgtgggaatc 2004
Qy 1984 tttttggctacgagacgctccattaaagtgaacagatcaacagatctcgtgtattgtg 2043
Db 2005 ttctctgttatgagaccagagtggttccactgagaagatcaatgatcacccggcgtgtg 2064
Qy 2044 ggcatagcatactaaacgttggtgtgcttctgtcgtataacagctcccggtgggcatgctc 2103
Db 2065 ggcattggtactacaaatgtggcagtcctgtgctcctcatcactgtctctgtcaccatgatt 2124
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Qy 2104 attgcatacgcaacagcagcgctcttctgtccttgccttgccttagctgtgatatctgtgtg 2163
Db 2125 ctgtccagcagcagagatgcagccttctgtccttgcctctcttgcctagtttctctctcc 2184
Qy 2164 ttctaagcatgctgctgatatattgtgccaaaggtcattgaggttatacgtcatcccccaag 2223
Db 2185 tatatacctcttctgtctcttctgtgccaagatgcgcaggctcgtatcaccacggaggaa 2244
Qy 2224 gataagccgaatcgaataacaatcccgattccagccatcgaagaaggagcagaagaacgc 2283
Db 2245 tggcagtcggagcgcagcagaccatgaagacagaggtcctcgaccaacaacaacagaggag 2304
Qy 2284 tatcagaaaacttgttaccgaaaacgacgaattgcaacgattataacacagaaggaggaa 2343
Db 2305 gagaagctccgctgttggagaaggagacccgtgaactggaaaagatcattgctgagaaa 2364
Qy 2344 aagattcgagctcgcgacagctc 2368
Db 2365 gaggagcgtgtctctgaactgcgc 2389

RESULT 5
AA58067
ID AAX58067 standard; cDNA to mRNA; 2602 BP.
XX
AC AAX58067;
XX
DT 21-JUL-1999 (first entry)
XX
DE Human GABAB receptor lj coding sequence.
XX
KW GABAB receptor; gamma aminobutyric acid type B receptor; inhibitor;
KW transient lower oesophageal sphincter relaxation; spasticity; emesis;
KW gastro-oesophageal reflux disease; epilepsy; psychiatric disorder; TLESR;
KW irritable bowel syndrome; dyspepsia; arthritis; allergy; diagnosis;
KW autoimmune disease; neoplastic disease; infectious disease; therapy;
KW alternative splicing; isoform; ss.
XX
OS Homo sapiens.
XX
PN W09921890-A1.
XX
PD 06-MAY-1999.
XX
PF 27-OCT-1998; 98WO-SE01947.
XX
PR 17-JUL-1998; 98SE-0002575.
PR 27-OCT-1997; 97SE-0003914.
PR 16-MAR-1998; 98SE-0000864.
XX
PA (ASTR ) ASTRA AB.
XX
PI Ekstrand J;
XX
DR WPI; 1999-302985/25.
DR P-PSDB; AAY14112.
XX
PT Polynucleotides encoding human and canine gamma aminobutyric acid
PT type B receptors, used to screen for compounds that are inhibitors
PT of transient lower oesophageal sphincter relaxations
XX
PS Example 7; Page 203-205; 222pp; English.
XX
CC This sequence encodes an isoform of a human gamma aminobutyric acid
CC type B (GABAB) receptor of the invention, created by alternate splicing.
CC Nucleic acid molecules encoding GABAB receptors can be used to screen for
CC compounds that are inhibitors of transient lower oesophageal sphincter
CC relaxations (TLESR). They can also be used to screen for agonists or
CC antagonists of the GABAB receptors. Inhibitors of TLESR are useful for
CC treating gastro-oesophageal reflux disease. Other uses of GABAB
CC receptors, such as human GABAB Rlc or ld, comprise diagnosis or treatment
CC of conditions related to GABAB dysfunction, e.g. epilepsy, psychiatric
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CC disorders, emesis, irritable bowel syndrome, dyspepsia, spasticity.
CC arthritis, allergies, autoimmune diseases, neoplastic diseases, pain and
CC infectious disease.
XX
SQ Sequence 2602 BP: 582 A; 737 C; 702 G; 581 T; 0 other;

Query Match 22.6%; Score 569.4; DB 20; Length 2602;
Best Local Similarity 54.8%; Pred. No. 4e-170;
Matches 1231; Conservative 0; Mismatches 981; Indels 33; Gaps 4;

QY	130	ccgatagccgcaagagagatgcaggcgccagcgctgtatgcctgccacaagactg	189	1115	gcaccgctggcctatgatgccatctctggcgcttggcactggccctgaacaagacatctgga	1174
DB	239	ctgtttcccatgagcggggctggccaggggccaggcgctgcagcccgcggtggaatg	298	1090	cgattgacaacccgggaagaaatctctgagggattttaccctatacggacagagagattgcc	1149
QY	190	gcgttgatgtgtcaacaagcagccgaatctgtgcggggttcaagctcatctctgcac	249	1175	ggagcgcgccgttctgtgtgcgctggaggacttcaacatacaacaacagaccattacc	1234
DB	299	gcgctggaagcgtgaatacgcgaggaacatctctgcggactatgagctcaagctcatc	358	1150	gatgaatctacgctgccatgaactcaacaatttctgggtgtatcggtgtggttgcca	1209
QY	250	agcaacgacagcgagtgtagcccggtttggcgccagcgtgtagtacaatctgctctat	309	1235	gaccaatctaccgggcaatgaactcttctcttggagggtctctctgccaatgtgtg	1294
DB	359	caccacgacagcaagtgtgaccaggccaagccaccaagtaacctatagctgtcttac	418	1210	ttcagttctcaggcgcatctattgtcttacacagatcgaaacagatgagacgccaag	1269
QY	310	aataaacgcaaaagctgactgttggcaggatgcagacggtctgaaccaactgtagcc	369	1295	tttgatgcagcggtctctcgatggcagcttatcgagcagcttcgggtggtgcagc	1354
DB	419	aacgacctataagatcatcttgcgtgctgagctgtgtctccacgctgtggtgct	478	1270	tacgaagaattgggttactacgatactcagttggataacctatactctgttgaatactgaa	1329
QY	370	gaggtgcacaaatgtgaatctaattgtctctgacggggtctgagtcgagtcgctctt	429	1355	tacaagaagattggtactatgacagcaacgaagatgatcttctctggtccaaacagat	1414
DB	479	gaggtgctagatgtggaacctattgtgtttctctatggctccagctcaccgccctg	538	1330	cadtgattggtggcaaggttcctcaagatcgcaaatgttcacccccattgttctacgacc	1389
QY	430	tcggatcgcaaacgattccccactctattccgcaccccatccatcgccacggtgcacaa	489	1415	aaatgattggagggtccccccagctgacacagacctggctcaacagacattccgcttc	1474
DB	539	tcaaacggcagcgtttcccactttcttcgaaacgcacccatcagccacactccaac	598	1390	gtgtccttcccatatttgtgtgcatgtgcacaatatccagttgtggcatatttgttgc	1449
QY	490	ccacgcgcatacagctgataaagaaatctcggtggttcccggttcccaattctgcagcg	549	1475	ctgtcacaaactcttatactccgtctcagttctctccagcttggcattgtctctagct	1534
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QY	550	gcggagaggtcttatagccgttagagatctcagaaatcagatcgatgagactgac	609	1535	gttgtctgtcttcccttaacatctacaactcacaatgcattgcgttatataccagaactcag	1594
DB	659	aceactgaggcttcaactcagctcagcactcgaggacctggaggacgagtgagctgga	718	1510	cccgtttgcaatcagatcatgttatttgggtgctcatctctgtctataatctctcatctta	1569
QY	610	gttgaatatgtaacatagacaatcttctccgatacacaagacgcggtgcgaatttg	669	1595	cccaactgaacaacctgactgctgtgggctgctcactgctttagctgtcttctcccc	1654
DB	719	attgagattacttccgcgagatttcttccagatccagctgtccgctcaaaaacctg	778	1570	ctgggcatcgacggagcgtttgtcagccccggaggaatatccaagaatagtccaagcgcg	1629
QY	670	cgacgcaggatgacgcacatctgtggactcttctctatgtgtgtggccgcaggggctg	729	1655	ctgggctcgatgttaccacattgggaggaacagttctctctcgtccagggccgc	1714
DB	779	aagcgccagatgccgaatcatcgtggacttttctatgagactgaagcccgaaagt	838	1630	gctgtgtactatccaccggtttacacgtagcatcagctgctatgttcagcaaggtctgg	1689
QY	730	ctctgcaaatgtcaaacacagcatatattggccgagctcatgtgtgttctttattggc	789	1715	ctctggctcctggcctggctttagctgtgggtcacggttccatgttccacaagaatttgg	1774
DB	839	ttttgtgagggtacaaggcgtctcttgggaagaagtacgtctgttctctcattggg	898	1690	cgtgtgcatcgttttacaacaa-----aagcaaaaactgaccacaagaaaaagtgtaa	1743
QY	790	tgttacgaggacaactggtacgaggtgaaatctgaaagcagagggcatcactcgtctgt	849	1775	tgggtccacacgcttctcaacaagaaggaagaaagaggtggaggagactctgga	1834
DB	899	tggTatgTgacaattgT-----tcaagatctacgaccttctatcaactgcacagt	952	1744	ccttggaaagctatacaccatgggttccgggctattatacaatagatttagtgataattact	1803
QY	850	gaacagatgcgaatagctgcgaaggacatctgacaacggaagcgctcatgttggaaatcg	909	1835	ccctggaagctgtatgccacagtggcgctgctgtgtggcatggatgtcctcactctcgcc	1894
DB	953	gatgagatgactgagcggttgaggggccacatcacaaactcagattgtcatgctgaatct	1012	1804	tcatggcagatcttgcacccgctgcagcgttatctcgaaacatccccactcgaaagatcca	1863
QY	910	aacaatcagacaactatataccgaatgactgcagagggaatttcgacatgcagtgaatcag	969	1895	atctggcagatctgtggacctctgcaccggaccattgagacatttgcgaaggaggaacct	1954
DB	1013	gccaatccccgcagacttccaacatgacatccccggaatttgtggaaacatacccaag	1072	1864	gtatctactactgatgatatataaatacgtccagagcttgagcattgtgaaagtcacagc	1923
QY	970	gcgctaactcgaggaggtttacgacattaaaccacgacgctatccccggaggatatcaggag	1029	1955	aaggaagatattgacg---tctctattctgccccagctggagcattgcagctccaggaag	2011
DB	1073	cgactgaaaagacacctgaggaga-----caggagggttccaggagg	1114	1924	aactccatgtggttgggtctgtatacggcttcaaggggctaactcctgggtgttggcgctc	1983
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				1984	tttttggcgtacgacgacgcgtccattaaagtgaacacagatcaacgattcgcgttatgtg	2043
				2072	ttccttgccttatgagaccaagagtgtgtccactgagaagataaatgatcaccggcgctg	2131
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				2104	attgcatcgcaacaggacgcgtctcttggccttggctgtctgtagctgtgatatctgtgtg	2163
				2192	ctgtccagccagcaggtatgcagccttggccttggcctctctcttgccaatagtttctctcc	2251

QY 2164 ttctaaagcgtgctgatatgttgcacaaaggctcattgaggttatatcgtcatcccaag 2223
 Db 2252 tataactctgtgtgctcttgtgcccagatgcgcaggtgatcccccagagggaa 2311
 QY 2224 gataagccgaatgaaatacaatccccgatccagccatcgcacatgcacaaagagacgaagacgc 2283
 Db 2312 tggcagtcggagggcgagacacacatgaagacaggttcacgacacaaacacagagag 2371
 QY 2284 tatcagaactgtttaccgaaacagagcaattgcacgattataacacagagagaa 2343
 Db 2372 gagaagtcctggctgttgagaagagacccgtgaactggaagaatcattgtgagaaa 2431
 QY 2344 aagattcagtcctgcagacagcgtc 2368
 Db 2432 gagagcgtgtctctgaactgcgc 2456

RESULT 6
 AAV10265
 ID AAV10265 standard; cDNA to mRNA; 2620 BP.
 XX AC AAV10265;
 XX DT 03-JUN-1998 (first entry)
 XX DE Human GABA-BR1a/b receptor cDNA.
 XX KW Gamma-aminobutyric acid; GABA-BR1a/b receptor; human; brain; agonist;
 KW inhibitory neurotransmitter; peripheral nervous system; antagonist;
 KW treatment; dementia; depression; anxiety; bronchial inflammation; asthma;
 KW epilepsy; cognitive function; ds.
 XX OS Homo sapiens.
 XX FH Key Location/Qualifiers
 XX CDS 1..2382
 XX FT /*tag= a
 XX FT /product= GABA-br1a/b
 XX PN W09746675-A1.
 XX PD 11-DEC-1997.
 XX PF 19-MAR-1997; 97WO-EP01370.
 XX PR 22-NOV-1996; 96US-0756091.
 XX PR 30-MAY-1996; 96US-0655716.
 XX PA (NOVS) NOVARTIS AG.
 XX PI Bettler B, Bittiger H, Froestl W, Kaupmann K, Mickel SJ;
 XX DR WPI: 1998-042183/04.
 XX DR P-PSDB; AAW40117.
 XX PT Purified GABA-B receptor or receptor protein - and antagonists of
 XX PT these which may be useful in treating nervous system disorders
 XX PS Claim 3; Page 56-62; 108pp; English.
 XX CC This cDNA sequence encodes a novel human GABA-B receptor protein,
 CC GABA-BR1a/b. GABA (gamma-aminobutyric acid) is the major inhibitory
 CC neurotransmitter found in the brain and peripheral nervous system
 CC and this receptor may be used for the identification of GABA-B
 CC receptor agonists and antagonists. Such proteins may be used in
 CC treatment of dementia, depression, anxiety, epilepsy, spasticity,
 CC bronchial inflammation or asthma or to improve cognitive function.
 CC GABA-B receptor ligands and probes derived from this sequence can be
 CC used to assay for GABA-B receptors or DNA encoding them.
 XX CC Sequence 2620 BP; 593 A; 716 C; 710 G; 601 T; 0 other;

Query Match 22.6%; Score 569.4; DB 19; Length 2620;
 Best Local Similarity 54.8%; Pred. No. 4e-170;
 Matches 1231; Conservative 0; Mismatches 981; Indels 33; Gaps 4;

QY 130 ccgataagccggaagagagatggcagggcgcggtgtatgctgcacacaaagactg 189
 Db 19 ctgtttcccatgagcggggtgcccagggccagcctccagccgcggtgagatg 78
 QY 190 gcgttgagatgtcaacaagcagccgaatctgtgcgggcttcaagctcatcctgcac 249
 Db 79 gcgtggagacgtgaatagccgaggaatcctgcggactatgctcgaactatgaactc 138
 QY 250 agcaacgacagcagtgtagcccggtttgggcgcagcagtgatgataactctctat 309
 Db 139 caccagacagcaagtgtatccaggccaagcccaagtaacctatgatgctgctac 198
 QY 310 aataaaccccaaaagctgctgttggcaggtgacgacgctctgcaccactgtagcc 369
 Db 199 aacgacctatcaagatcattccttatgctggtgcagctgtctccacgctggtgct 258
 QY 370 gaggtgcgcaaaatgtggaatctaatgtgctgtctgctacggggcctcgagtccggtctt 429
 Db 259 gaggtgctaggtgtggaacctcatgtgttctctatggtccagctcaccagcctg 318
 QY 430 tcggatgcgaacagattccccactctattccgacccatccatccatcggccacggtgcacaa 489
 Db 319 tcaaacggcagcgtttccccactttcttcgaaacgaccatcagccacactccacaac 378
 QY 490 ccaacgcgcatcaagctgtagaataattcgctgttccgggtggtccattctgcacag 549
 Db 379 cctaccgcgtgaaactcttgaagggtgggctggaagaatgctgctaccatccacag 438
 QY 550 gcggagaggtcttattatcgacogtagaggtatctcgagaatcgtcatgaggtggc 609
 Db 439 accactgaggtcttctacttgcactctggacacctggaggaacgaggaagaggtcga 498
 QY 610 gttgaaatcgtaactagacaatttctatccgatacgaacgacgcgtgcgaatttg 669
 Db 499 attgagattacttccgcagagtttctctcagatcagctgtgcccgtcaaaactcg 558
 QY 670 cgacccagatgcacgcatcttgtggagcttctatgtgtggtgcccgcagaggtg 729
 Db 559 aagcgcaggtgcccgaatcctggtggacttcttctatgagctgaagccggaagt 618
 QY 730 ctctgcgaaatgtacaaacagcagctatatggcgaagctcatgtgtgttttatggc 789
 Db 619 ttgtgaggtgtacaagagcgtctcttgggaagaagtacgtgtgttctctcattggg 678
 QY 790 tggtagcaggaactggtacaggtgaaatctgaaagcagagggcatcactgactgtt 849
 Db 679 tggtagctgacaattggt-----tcaagatctacgaccttctatcaactgcacagt 732
 QY 850 gaacagatgcgaatagctgcggaaggacatctgcacaggaagcgtcatgtggaatcag 909
 Db 733 gatgagatgactgagcgtgtggagggccacatcacaactgagattgtctgtaacct 792
 QY 910 acaatcagacaactatattccggaatgactgcagagaatttcacatgcactgaatcag 969
 Db 793 gccaatcccgcgccatttcccaatgacatcccggaattgtggaactaaccaag 852
 QY 970 gcgctaactgagaggtttacgcattaaaccagctcgtatccgagggggataccagg 1029
 Db 853 cgactgaaagacacctgaggaga-----caggaggttccaggag 894
 QY 1030 gcgccaactgcctacatgacgtggtgaggtgtggtgttggcttcaacaagacctgaa 1089
 Db 895 gcaccgtggtcctatgatgccattggccttggcactggcctgaaacagacatctgga 954
 QY 1090 cgattgacaaccggggaagaaatctctgagggattttacattacatcggaagagattgcc 1149
 Db 955 ggaggcggccgttctgtgtgctgaggtgacttcaactacaacaaccagaccattacc 1014


```
Db 2449 gagaagtcctccgctgttggaagagagaaacgtgaactggaagaaagtattctgctgaaaa 2508
QY 2344 aagattcagtcctgcgcacagctc 2368
Db 2509 gaggagcgtgtctctgaactgcgc 2533

RESULT
AAX58062
ID AAX58062 standard; cDNA to mRNA; 2700 BP.
XX AC
XX AAX58062;
XX
XX 21-JUL-1999 (first entry)
XX
XX Human GABAB receptor le coding sequence.
XX
XX GABAB receptor; gamma aminobutyric acid type B receptor; inhibitor;
XX transient lower oesophageal sphincter relaxation; spasticity; emesis;
XX gastro-oesophageal reflux disease; epilepsy; psychiatric disorder; TLESR;
XX irritable bowel syndrome; dyspepsia; arthritis; allergy; diagnosis;
XX autoimmune disease; neoplastic disease; infectious disease; therapy;
XX alternative splicing; isoform; ss.
XX
XX Homo sapiens.
XX
XX WO9921890-A1.
XX
XX 06-MAY-1999.
XX
XX 27-OCT-1998; 98WO-SE01947.
XX
XX 17-JUL-1998; 98SE-0002575.
XX 27-OCT-1997; 97SE-0003914.
XX 16-MAR-1998; 98SE-0000864.
XX
XX (ASTR ) ASTRA AB.
XX
XX Ekstrand J;
XX
XX WPI: 1999-302985/25.
XX P-PSDB: AAY14107.
XX
XX Polynucleotides encoding human and canine gamma aminobutyric acid
XX type B receptors, used to screen for compounds that are inhibitors
XX of transient lower oesophageal sphincter relaxations
XX
XX Example 7; Page 162-168; 222pp; English.
XX
XX This sequence encodes an isoform of a human gamma aminobutyric acid
XX type B (GABAB) receptor of the invention, created by alternate splicing.
XX Nucleic acid molecules encoding GABAB receptors can be used to screen for
XX compounds that are inhibitors of transient lower oesophageal sphincter
XX relaxations (TLESR). They can also be used to screen for agonists or
XX antagonists of the GABAB receptors. Inhibitors of TLESR are useful for
XX treating gastro-oesophageal reflux disease. Other uses of GABAB
XX receptors, such as human GABAB R1c or 1d, comprise diagnosis or treatment
XX of conditions related to GABAB dysfunction, e.g. epilepsy, psychiatric
XX disorders, emesis, irritable bowel syndrome, dyspepsia, spasticity,
XX arthritis, allergies, autoimmune diseases, neoplastic diseases, pain and
XX infectious disease.
XX
XX Sequence 2700 BP; 599 A; 764 C; 741 G; 596 T; 0 other;

Query Match 22.6%; Score 569.4; DB 20; Length 2700;
Best Local Similarity 54.8%; Pred. No. 4.le-170;
Matches 1231; Conservative 0; Mismatches 981; Indels 33; Gaps 4;

QY 130 ccgatagccgcgaaggaggtggcaggcgccaggcggtgtatgctgctgcccaagactg 189
Dp 337 ctgtttcccatgagcgggggctggccagggggcccaggccctgcagcccggtggagatg 396
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QY 190 gccttgatgatgtcaaaagcagccgaaatctgtgccgggttcaagctcatctcgtcac 249
Db 397 gcctggaggagcgtgaatagccgaggaatcctcgcgactatgactcaagctcatc 456
QY 250 agcaacgacagcagtgtagcccggtttgggcccagcgtgtagtaacattctctctat 309
Db 457 caccacgacagcagtgtagcccggtttgggcccagcgtgtagtaacattctctctac 516
QY 310 aataaacccgcaaaagctgtagtggtggcaggaatgcagcagcgtctcaccactgtgacc 369
Db 517 aacgacctatcaagatcatccttatcctggtgcagctctgtctccacgctggtggt 576
QY 370 gagggtgccaaaatgtggaatctaattgtctctgtctacaggggctcagtcgggtctct 429
Db 577 gagggtcgtagtgtaggaacctcatgtgtcttctatggtccagctcaccagccctg 636
QY 430 tcggatgcgaacagattcccccactctattccgaccacatccatcgccacaggtgcacaa 489
Db 637 tcaaacggcagcgttttcccactttctccgaacgacccatcagccacactcacaac 696
QY 490 ccaacgcgcacatgtaggaagaattcggctgtggtcccggtggccattcttcagcag 549
Db 697 cctaccgcgtgaacctcttgaaaagtggggtcgggaagattgtctacatccagcag 756
QY 550 gcggaggaggtctttatatcgaccgtgaggaatctcagaaatcgatgcatggagctggc 609
Db 757 accactgaggtcttctcacttcgactcgtgagcactgaggaacgagtgaaggagctgga 816
QY 610 gtgaaatcgtaaactagacaaatcttctatccgatccaaacagacgcgtgcgcaattg 669
Db 817 attgagattacttccgccagagtttctctcagatcagcgtgtgcccacaaacctg 876
QY 670 cgacgcaggaatgcacatcattgtggactcttctatgtgtggccgcagaggggtg 729
Db 877 aagcgcaggaatgccgaatcactcgtggactttctatgagactgaagcccgaaagctt 936
QY 730 ctctcgaaaatgtacaaacagcagctatattggccgagctcactgtgtgtttttattggc 789
Db 937 tttgtgaggtgtacaaggagcgtctcttgggaagaagtacgtctgtgttctcatggg 996
QY 790 tggtagcaggaacaaactggtacgaggtgaatctgaaacagagggcaccatccactgactgt 849
Db 997 tggtagtgcacaattggt-----tcaagatctacaccttctatcaactgacagtg 1050
QY 850 gaacagatgcgaatagctgcggaaggacatctgacaacggaagcgtcatgtgaaatcag 909
Db 1051 gatgagatgactgagggcgtggaaggccacatccactgagattgtctatgctgaatcct 1110
QY 910 aacaatcagacaactatccggaatgactgcagaggaaatttcgacatcgactgaatcag 969
Db 1111 gccaataccgcagcatttccaaatgacatcccaggaatttgggaaactaaccaag 1170
QY 970 gcgctaactcagaggggttaacgacattaaacacgactcgtatccggagggtatcagag 1029
Db 1171 cgactgaagaacacctgaggaga-----caaggaggcttccagag 1212
QY 1030 gcgccactccctacagatgcaggtgagtggtggttggcttttcaacaagacatggaa 1089
Db 1213 gcaccgctgcctatgatgcactctggccttggcactggccctggaacagacatcggga 1272
QY 1090 cgatgacaaccgggaagaatctctgagggttttacctatgcggaacagagatgccc 1149
Db 1273 ggaggcgccgttctgtgtgctgaggaacttcaactacaacacagaccattacc 1332
QY 1150 gatgaatctacgctgccatgaactccacaaatttctgggtgtatcggtgtgtggca 1209
Db 1333 gaccaaataccgggcaatgaactcttctgcttgggggtgtctctggcactgtggtg 1392
QY 1210 ttcaattctcagggcgtatgtattgtctcttacacagatcgaacagatgataagacggaag 1269
Db 1393 ttgtatgccagcgtctcgtcgtggtgacgttatcagagcagcttcaagggtggcagc 1452
```


QY	1270	tacagagaagttggtttactacagactactcagtttggaataacctatctcctggttgaataactgaa	1329
Db	1453	tacaagaagattggctactactgacagcaccagagtgatctcttccttggtcccaaacagat	1512
QY	1330	cagtggaattggtggcaaggttcctcaagatcgcaaatgtcaacccatgttctacgcacc	1389
Db	1513	aaaaggattggagggtcccccacagctgaccagacctgtctatcagaacatctccgttc	1572
QY	1390	gtgtcttgccattattttgtgtgcattgacaaatcaccattgtgtgcattatcgttgcc	1449
Db	1573	ctgtcaagaacactttatctccgtctcagttctctccagctgggcattgtctctagct	1632
QY	1450	ttcgccttgatcatctttaatatatggaaataagcatagaagagtaatacaaatctcgcgat	1509
Db	1633	gtgtctgtctgtctttaaacatctacaactcacatgtccgtttataccagaacatcacag	1692
QY	1510	cccgtttgcaatacagatcatgttatttgggtgctcatcatctgtctataatctgtcatctta	1569
Db	1693	cccaactggaacaacctgactgctgtgggtgctcactggttttagctgctgtctctccc	1752
QY	1570	ctgggcatcgagcagcgttttgcagccccggaggaaatctccaaagatatgtcaagcgcgg	1629
Db	1753	ctggggtctgatgtgtacacaattgggaggaccaggttctcttctgtcgcaggcccgc	1812
QY	1630	gcttgggttactatcacccggttttacactagcatcacggtgctatgtgttcagcaagctctgg	1689
Db	1813	ctctgggtccctgggcctgggtctgttagtctctgggtcactggttccatgttccaagaattgg	1872
QY	1690	cgtgtgcatcgtttttacaaaca-----aagcaaaaactgaccccaagaaaaaagtggaa	1743
Db	1873	tgggtccacacggtctctcacaaagaaggaaagaaagagggtggaggaagactctggaa	1932
QY	1744	cttgggaagctatacaccatggttttcggggtattatcaataagattagattagtattactc	1803
Db	1933	cccgtggaaagctgtatggccacagtgggccctgtgcggggcatgggtgtctctcatctcggc	1992
QY	1804	tcatggcagatctttgatccgctgcagcgtttatctcgaaacattcccactcgaagatcca	1863
Db	1993	atctgggcagatcgaggacccctctgcacggaccatttgacatttgccaaggaggaaacct	2052
QY	1864	gtatctactactgatgattataaaatacgtccagagcttgacgattgtaaaagtcacaagc	1923
Db	2053	aaggaagatatggacg---tctctattctgcccacgctggagcattgacgtccagcgaag	2109
QY	1924	aactccatgtggttgggtctgtgtacagcttcacagggctcaagggctaatcctggtttgccc	1983
Db	2110	atgaatacatgcttggcattttctatggtttacaaggggctgctgctgtcgtcgtcgtggaatc	2169
QY	1984	tttttggcgtacagagcgcgtcccatataagtgaaacagatcaacgattcgcgtttatgtg	2043
Db	2170	ttcctgtcttatgagaccagaagtggtgtccactgagaagatcaatgatcacgggctgtg	2229
QY	2044	ggcatgagcatctataacggtgggtcgtctcttggcctgataaacgctccggttgggcattggtc	2103
Db	2230	ggcatggtctatcacaattggcagtcctgtgctctcatcactgctgctgtcactcatgatt	2289
QY	2104	attgatcgcgaacaggacgcgtctttgcccctgtgtgtctctagctgtgattctgttgt	2163
Db	2290	ctgtccagccagcaggaagcagcctttgcccctgtgtctctctgtcctctctgtccatagtttctcctcc	2349
QY	2164	ttcttaagcatgctgctgatattgtgcccaggctcattggaggtttatcgtcatcccaag	2223
Db	2350	tatacactctgtgtgtctcttgtgtcccaagaatgcgcaggtgatcacccgaggggaa	2409
QY	2224	gataaggccgaatcgaaatacaatccccgattcagccatatcgaagaggagacgaagaagc	2283
Db	2410	tggcagtcggaggcgcagaccatgaagacaggggtcatcgaccacaacacacagagag	2469
QY	2284	tatcagaacctgttacggaaaaacagcaattgcaacgatttaatacacagaagaggaa	2343
Db	2470	gagaaggctcccgccgttgggaaggaagcccgtagactggaaagatcatctgtcgagaa	2529
QY	2344	aagattcaggtccttgcgacagcgtc	2368

Db	2530	gaggagcgtgtctctgaactgcgc 2554	
RESULT	9		
AAZ35410			
ID	AAZ35410	standard; cDNA; 2822 BP.	
XX	AC	AAZ35410;	
XX	DT	27-MAR-2000 (first entry)	
XX	DE	Human G-protein coupled receptor GABAB1b cDNA.	
XX	KW	GABAB1b; G-protein coupled receptor; human; *antibacterial;	
KW	KW	antiviral; virucide; antiparasitic; analgesic; cytostatic;	
KW	KW	antidiabetic; anorectic; cardiast; antiparkinsonian;	
KW	KW	hypertensive; hypotensive; antiemetic; osteopathic; antianginal;	
KW	KW	cerebroprotective; antiulcer; antiallergic; neuroleptic;	
KW	KW	tranquillizer; antidepressant; nootropic; antimigraine;	
KW	KW	anticonvulsant; neuroleptic; agonist; antagonist; inhibitor;	
XX	KW	therapy; diagnosis; ss.	
XX	OS	Homo sapiens.	
XX	FH	Key Location/Qualifiers	
FT	CDS	49..2583	
FT	FT	/*tag= a	
XX	PN	W09958567-A1.	
XX	XX	18-NOV-1999.	
XX	XX	03-MAY-1999; 99WO-US09655.	
XX	XX	08-MAY-1998; 98US-0075463.	
XX	PA	(SMK) SMITHKLINE BEECHAM CORP.	
XX	XX	Elshourbagy NA, Halsey WS;	
PI	PI	WPI; 2000-116287/10.	
XX	XX	P-PSDB; AAY32467.	
DR	DR		
PT	PT	New human GABAB1b polypeptides and polynucleotides used to identify	
XX	XX	agonists, antagonists and inhibitors for use in therapy	
XX	XX	Claim 2; Page 33-35; 46pp; English.	
XX	XX	This is the nucleotide sequence of human cDNA coding for the	
CC	CC	G-protein coupled receptor GABAB1b (see AAZ32456). The cDNA was	
CC	CC	obtained by PCR amplification (see AAZ35411-12) using brain cDNA as	
CC	CC	template. The invention provides GABAB1b polypeptides and	
CC	CC	polynucleotides, and methods for producing such polypeptides by	
CC	CC	recombinant methods. GABAB1b polypeptides may be used for	
CC	CC	identifying agonists and antagonists/inhibitors, and for detecting	
CC	CC	diseases associated with inappropriate GABAB1b activity or levels	
CC	CC	GABAB1b polypeptides and polynucleotides, agonists, antagonists and	
CC	CC	antibodies are used to treat bacterial, fungal, protozoan and viral	
CC	CC	infections, particularly HIV-1 and HIV-2, pain, cancer, diabetes,	
CC	CC	obesity, anorexia, bulimia, asthma, Parkinson's disease, acute	
CC	CC	heart failure, hypotension, hypertension, urinary retention,	
CC	CC	osteoporosis, angina pectoris, myocardial infarction, stroke,	
CC	CC	ulcers, allergies, benign prostatic hypertrophy, migraine,	
CC	CC	vomiting, psychotic and neurological disorders including anxiety,	
CC	CC	schizophrenia, manic depression, depression, delirium, dementia and	
CC	CC	severe mental retardation, and dyskinesias such as Huntington's or	
CC	CC	Gilles de la Tourette's syndrome. The polynucleotide is also	
CC	CC	useful as a source of primers and probes, and for detecting the	
CC	CC	above diseases.	
XX	XX	Sequence 2822 BP; 612 A; 820 C; 760 G; 630 T; 0 other.	

Qy 2344 aagattcgagtcctgcgacagcgtc 2368

Query Match		22.6%;	Score 569.4;	DB 21;	Length 2822;
Best Local Similarity		54.8%;	Pred. NO. 4.2e-170;		
Matches 1231;		Conservative 0;	Mismatches 981;	Indels 33;	Gaps 4;
QY	130	ccgatagccgcaaaaggaggtgagcagggccagggcgtgtatcctgccacaagactg	189		
DB	220	ctgtttcccatgagcggggctgccaaggggccggcctgcagcccggtggagatg	279		
QY	190	gcgttgatgatgtcaacaagcagccgaatctgctgccgggttcaagctcatcctgcac	249		
DB	280	gcgctggagcagtgaaatagccgaggaacatcctgcggactatgagctcaagctcac	339		
QY	250	agcaacagcagcaggtgagcccggttggggccagcagtgatgtacaatatgtctctat	309		
DB	340	caccacagcagcaggtgtatccaggccaagccaccaagtacctatatgactgtctctac	399		
QY	310	aataaacgcgaagactgaatctgttggcagatcagcacggtctgcacactgtagcc	369		
DB	400	aacgacctatacaagatcatccttatgctggctggcagctgtctccacgctgg	459		
QY	370	gagctgcgaataatggaataatgtgctctgctacggggcctcgagtcggctctt	429		
DB	460	gagctgtagatgtgaaactcatgtgttctctatgctccagctcaccagccctg	519		
QY	430	tcgcatcgaacagattcccaacttatccgcacccatccatcgccacggtgcacaat	489		
DB	520	tcaaacggcagctttcccaactttctccgaacgcacccatcagcacactccacaac	579		
QY	490	ccaacgcgcataagctgatgaagaaatcgctgctcccggtggtccattctgcagcag	549		
DB	580	cctaccgcgtgaaactcttggaaagtggggctgggaagatgtgtaccaatccagcag	639		
QY	550	gcggaggaggtctttaatcgaccgtagaggatctcgaaatcgatgcatggaggtcgc	609		
DB	640	accataggcttcacattcgactctgacgacctggagaaacgagtgaaaggactgga	699		
QY	610	gttgaatcgtaaactagacaatcatctctatccgatacccaacagcgcgtgcgaattg	669		
DB	700	attgagattactttccgcagaggtttcttctcagatccagctgtgcctcaaaaacctg	759		
QY	670	cgacgcagagatgcacatctgtggactcttctatgtggtggcccccagagggtg	729		
DB	760	aagcgcaggatgcgccgaatcatcgtggactttctctatgactgaagcccggaaagt	819		
QY	730	ctctgcgaatgtcaaacagcagctatatggcgcagctcatgtgtggttctttattgc	789		
DB	820	tttgtgaggtgtacaaggagcgtctcttgggaagaagtagctgtgttctctattggg	879		
QY	790	tgttacgaggacaactgtgacgaggtgaatctgaaagcagagggtcatcacctgcactgt	849		
DB	880	tggatgctgacaattggt-----tcaagatctacgaccttctatcaactgcacagt	933		
QY	850	gaacagatgcgaatagctgcggaagacaatctgacaacggaagcgtcatgtggaaatcag	909		
DB	934	gatgagatgactgagcgggtggagggccacatcaacaactgagattgtcatgctgaatcct	993		
QY	910	aacaatcagacaactatataccggaatgactgcagaggaaatttcgacatcgactgaatcag	969		
DB	994	gccataccgcagcatttccaaatgacatcccgggaatttgggagaaactaaccaag	1053		
QY	970	gcgctaactcgagggtttacgacattaacccagcatcgctatccggagggtatcaggag	1029		
DB	1054	cgaactgaaagacacccctgaggaga-----caggaggttccaggag	1095		
QY	1030	gcgcgaactcgcactagatgcaggtgtggaggtgtgggtttggcttcaacaagacctgga	1089		
DB	1096	gcacgcgtggcctaigtatccatctgggcttggcactggcctggaacaagacatctgga	1155		
QY	1090	cgattgaacaccgggaagaaatctctgagggtatttacctatcagggaagagattgcc	1149		
DB	1156	ggagggcggcttctgtgtgctgtgaggacttcaactacaacaacacagaccattacc	1215		

QY	1150	gatgaaatctacgctgccatgaaactccacacaaatttctgggtgtatcgggtgtgtggca	1209		
DB	1216	gaccaaatctaccgggcaatgaactcttcgtctttgagggtgtctctggccatgtgtg	1275		
QY	1210	ttcagttctcagggcgcgtatgtattgtcttacacagatcgaacagatgatagacggcaag	1269		
DB	1276	tttgatgccaagcgtctcggatggcatggacgcttatccagacagcttcagggtggcagc	1335		
QY	1270	tacgagaagtgggtttactacgatactcagttggataacctatcctcgttgaatactgaa	1329		
DB	1336	tacaagaagattggctactatgacagcaccaaggatgatctttcctggtccaaacagat	1395		
QY	1330	cagtggaattggtagcaaggttcctcaagatgcgcacaattgtcaaccatgttctacgacc	1389		
DB	1396	aaatggattggaggttccccccagctgaccagacctggctcaacaagacattccgcttc	1455		
QY	1390	gtgtccttgccattatttgtgtcatgtgcacaatatccagttgtggcatattcgttgcc	1449		
DB	1456	ctgtcaagaacctttatctcctgttcaggtctctccagcctgggcatgtgctcagct	1515		
QY	1450	ttcgcttgatcatcttttaatatatggaataagcatagaagagtaatacacaatcctcgcat	1509		
DB	1516	gttgtctgtctgtctttaacatcacaactcacatgctccgttatataccgaactcacag	1575		
QY	1510	ccggttgcaatacagcatcatgttatttgggtgcatcatcgtcttaataatcgtcatctta	1569		
DB	1576	cccaacctgaacaacctgactgctgtgggtgctcactggctttagctgtgtcttcccc	1635		
QY	1570	ctgggcatcgacgacgactttgtcagccccgaggaaatatacgaagatgtccaagcgcg	1629		
DB	1636	ctggggctcgatggtttaccacatgggaggaaacagtttctcttcgtctgccagggccgc	1695		
QY	1630	gcttggttactatccaccggttttacactagcatcacggtgctatgttcagcaaggtctgg	1689		
DB	1696	ctctggctcctggcctggcctttagctctgggtacaggttccatgttccaccaagattgg	1755		
QY	1690	cggtgcatcgttttacaacaa-----aagcaaaactgacccaagaagaaaaagtgga	1743		
DB	1756	tgggtccacacggtcttcaacaagaagaaagaagaggtggaggaaagactctggaa	1815		
QY	1744	ccttggagcatatacacatcaggttttcgggctattatcaatagatttagtattactc	1803		
DB	1816	ccctggagctgtatgcccacagtgggcgtgctgtgggca tggatgtcctcactctgccc	1875		
QY	1804	tcatggcagatctttgacccgtcagcgtttatctcgaaacatctccactcgaaagatcca	1863		
DB	1876	atctggcagatcgtggaccctctgcacggaccattgagacatttgcgaaggagaacct	1935		
QY	1864	gtatctactactgatataataaatacgtccagagcttgagcatttgaaagtcaaacgc	1923		
DB	1936	aaggaaatattgacg---tctctattctgccccagctggagcattgcagctccagggaag	1992		
QY	1924	aactccaatgtgtgggtcttgtatagcgttcaaggggttaactcctcgtgttttgccctc	1983		
DB	1993	atgaatacatggcttggcattttctatggttacaagggtcgtgctgctcgtgggaatc	2052		
QY	1984	tttttggcgtacgacgacgcgtcccatataaagtgaacacagatcaacgattcgcgttatgtg	2043		
DB	2053	ttccttcttatgagaccaagagtggttccactgagaagatcaaatgatcaacgggctgtg	2112		
QY	2044	ggcatgagcatctataacgtgggtcgtcctttgcctgataacagctcccggtgggcatggtc	2103		
DB	2113	ggcatggctatcaaatgtggcagctcgtgtcctcatcactgctcctgtcaccatgatt	2172		
QY	2104	attgcatcgcaaacaggacgcgtccttgccttgcctcgtctcgtatgctgtattctgtgt	2163		
DB	2173	ctgtccagccagcaggtgcagccttgcctttgcctctcttgcctatgattttctctccc	2232		
QY	2164	ttcctaagcatcgtcgtgatatattgtccaaagctcatttgagggttatcagtcacatcccaag	2223		
DB	2233	tatatcactctgtgtgtcgtcttgtgtcccaagatgcgaggtcgtgatcccccgggggaa	2292		
QY	2224	gataaggccgaatcgaaatacaatcccgaattcagcccatatcgaaaggaggaagaagcgc	2283		

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Db 2293 tggcagtcgagcgagacacacatgaagacagaggtcatcgaccacacacagagag 2352
QY 2284 tatcagaatactgttaccgaaacagcaattgcaacgattataacacagagagagaa 2343
Db 2353 gagaagtcceggctgttgagaaagagacacgtgaactggaagaagatcatctgagaaa 2412
QY 2344 aagattcagtcctgcgacagcgtc 2368
Db 2413 gaggagcgtgtctgtaactgcgc 2437

RESULT 10
AAZ06970
ID AAZ06970 standard; cDNA; 2886 BP.
XX AC
XX AAZ06970;
XX DT
XX 15-NOV-1999 (first entry)
XX DE
XX Human gamma-amino-butyric acid B receptor subunit GABABR1a cDNA.
XX KW
XX Gamma-amino-butyric acid B receptor subunit; HG20; GABABR1a;
XX KW depression; epilepsy; neuropsychiatric disorder; dementia;
XX KW muscular contraction; central nervous system disorder; ss.
XX OS
XX Homo sapiens.
XX FH
XX Key Location/Qualifiers
XX CDS 1..2886
XX FT /*tag= a
XX FT /product= "GABABR1a"
XX FT /note= "gamma-amino-butyric acid B receptor subunit"
XX PN
XX WO9940114-A1.
XX PD
XX 12-AUG-1999.
XX PF
XX 03-FEB-1999; 99WO-US02361.
XX PR
XX 05-FEB-1998; 98US-0073767.
XX PA
XX (MERI ) MERCK & CO INC.
XX PA (MERI ) MERCK FROSST CANADA INC.
XX PA (UYTE-) UNIV TEXAS HEALTH SCI CENT SAN ANTONI.
XX PA (USSH ) US NAT INST OF HEALTH.
XX PI
XX Bonner TI, Bonner TP, Clark J, Kolakowski LF, Liu Q;
XX PI McDonald T, Ng GYK;
XX PP
XX WPI; 1999-527300/44.
XX DR
XX P-PSDB; AAY29798.
XX XX
XX New DNA encoding human and murine receptor subunits, useful for
XX PT identifying agonists and antagonists for treatment of depression,
XX PT epilepsy and neuropsychiatric disorders
XX XX
XX Disclosure; Fig 18; 128pp; English.
XX XX
XX The present sequence encodes a human gamma-amino-butyric acid (GABA)
XX CC B receptor (GABABR) subunit designated GABABR1a. The present invention
XX CC also describes the GABABR subunit designated HG20. Cells expressing
XX CC the new receptor subunits are useful for identifying GABABR agonists
XX CC and antagonists. HG20 proteins and their antagonists are useful for
XX CC inhibiting HG20 or GABABR function, useful for treating depression,
XX CC epilepsy, neuropsychiatric disorders, dementias, muscular contractions,
XX CC and central nervous system disorders.
XX XX
XX Sequence 2886 BP; 632 A; 822 C; 797 G; 635 T; 0 other;
SQ

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Query Match 22.6%; Score 569.4; DB 20; Length 2886;
 Best Local Similarity 54.8%; Pred. No. 4.3e-170;

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Matches 1231; Conservative 0; Mismatches 981; Indels 33; Gaps 4;
QY 130 ccgataccggcgaagagagatggcaggcgccaggcggtgtatctgtccacagactg 189
Db 523 ctgttcccattgagcggggctggccaggggccaggcctgccaggccgggtgagatg 582
QY 190 gcgttgatgatgtcaaacagcagccgaatctgtcgcgggttcaagctcatctgcac 249
Db 583 gcgtggagacgtgaatagccgagggacatcctgcggactatgagctcaagctcatc 642
QY 250 agcaacgacagcagtgtagcccggtttggcgccagcgtgtagtatacaactctgctat 309
Db 643 caccacgacagaagtgtgattccaggccaagccaagtaacctatatgactgctctac 702
QY 310 aataaacccgcaaaagctgtagtctgtggcaggatgcagcagcgtgtgcacacgttagcc 369
Db 703 aacgacctatcaagatcatccttatgctgtgcagctctgtctccacgctgtggtct 762
QY 370 gaggctgccaaaatgtggaatctaattgtctctgtctacaggggcctcgagtcggctctt 429
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QY 430 tcggatcgcaaacgattcccaactctattccgcaacctcatcgcacaggtgcacaaat 489
Db 823 tcaaacggcagcgtttcccaacttttccgaaacgaccccatcagccacactccacaac 882
QY 490 ccaacgcgcatacagctgatgaagaaatctggctgtgctccgggtggccattctgcagcag 549
Db 883 cctaccgcgctgaaacctttgaaaagtggggctggaagaagattgtctaccatccagcag 942
QY 550 gcggagaggtctttatagccgctgagagatctcgagaatcgatgcattgagagctggc 609
Db 943 accactgaggtcttcaactctgactctgagcagcctgagggaacgagtggaagagctgga 1002
QY 610 gtgaaatcgtaaactagacaatcatttctatccgatccacagcgcgtgcgaatttg 669
Db 1003 attgagattactttcccgagagtttcttccagatccagctgtgcccgtcaaaaacctg 1062
QY 670 cgacgccagatgcacgcacatcattgtgggactcttctgtggtggccgcagagaggtg 729
Db 1063 aagcgcagatgccgaatcatcgtgggacttttctatgagactgaagcccgaaagt 1122
QY 730 ctctggaatgtacaacagcagcttatatggccgagctcatgtgtgtgtttttatggc 789
Db 1123 tttgtgaggtgtacaaggagcgtctctcttgggaagaagtacgtgtgttctcatggg 1182
QY 790 tgtacgagacaactgtgtacgaggtgaatctgaaagcagagggcaccactgcactgtt 849
Db 1183 tggtagctgacaattgggt-----tcaagatctacgaccttctatacactgcacagt 1236
QY 850 gaacagatgcgaatagctgcgaaggagacatctgacaacggaagcgtcatgtggaatcag 909
Db 1237 gatgagatgactgagcgtggaggccacatcaacactgagattgtcatgtgaatcct 1296
QY 910 acaatcagacaactatataccggaatgactgcagaggaatttcgacatcgactgaatcag 969
Db 1297 gccaataccgcgacatttccacatgacatcccaggaatttgggaaactaaccag 1356
QY 970 gcgctaactcgagaggggttacgacattaaaccaagatcgctatccgagggaatacagag 1029
Db 1357 cgactgaaagacacctgaggaga-----caggaggtctccaggag 1398
QY 1030 gcgccactgcctacatgcagtgtagtggtgtggtgtggttttccacaagacctgaa 1089
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QY 1090 cgattgacaacccgggaagaaatctctgagggattttacctatacgcgagggagatgcc 1149
Db 1459 ggaaggcgcgttctgtgtgctgcctggaggacttcaactacaacacagaccattacc 1518
QY 1150 gatgaatactacgtgccatgaactcaacacaaatttctgggtgtatcggtgtggtggca 1209
Db 1519 gaccaaatactaccgggcaatgaactctctgctcttgagggtgtctctgcccattggtgtg 1578

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Db 2716 gagagcgtgtctctgaactgcgc 2740
RESULT 12
AAx90921
ID AAX90921 standard; DNA; 2887 BP.
XX
AC AAX90921;
XX
DT 17-JAN-2000 (first entry)
XX
DE Human GABABR1b receptor subtype DNA.
XX
KW GABABR1b receptor protein; cloning; rat brain; GABABR2; GABAB receptor;
KW human gamma-aminobutyric acid receptor; metabotropic receptor; screening;
KW synaptic transmission; GABABR1b; cloned receptor; splice variant;
KW modulatory agent; molecular activity assay; antispastic; anti-addictive;
KW antineurodegeneration; analgesic; cardiovascular activity; ds.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 1..2535
FT FT /*tag= a
FT FT /product= "Human GABABR1b receptor protein"
XX
PN W09951636-A2.
XX
PD 14-OCT-1999.
XX
PE 02-APR-1999; 99WO-US07352.
XX
PR 03-APR-1998; 98US-0080676.
XX
PA (NPSP-) NPS PHARM INC.
XX
PI Garrett JE, Simin RT, Busby JG, Stormann TM;
XX
DR WPI; 1999-610994/52.
DR P-PSDB; AAY28839.
XX
XX Novel nucleic acids, used to screen for specific modulators, e.g. for
XX treating spasticity or Alzheimer's disease -
XX
XX Disclosure; Fig 1A-1L; 78pp; English.
XX
XX The present sequence encodes GABABR1b receptor protein cloned from rat
XX brain. This is closely related to GABABR2. GABAB receptors are
XX metabotropic receptors that modulate synaptic transmission in brain.
XX GABABR1a differs from GABABR1b in that the N-terminal 147 residues are
XX replaced by 18 amino acids. Both of these cloned receptors appear to be
XX splice variants. They are expressed in cells that express GABABR2. This
XX nucleotide sequence is used to screen for specific modulators. These
XX modulators have antispastic, antineurodegeneration, analgesic, anti
XX -addictive, cardiovascular activities.
XX Note: SEQ ID NO. 8 is referred as the GABABR1a receptor protein in
XX the specification.
XX
XX Sequence 2887 BP; 624 A; 823 C; 776 G; 664 T; 0 other;
XX
Query Match 22.6%; Score 569.4; DB 20; Length 2887;
Best Local Similarity 54.8%; Pred. No. 4.3e-170;
Matches 1231; Conservative 0; Mismatches 981; Indels 33; Gaps 4;
QY 130 ccgatagccgcaagaggatggcaggcgccaggcggtgtatgcctgcccacaagactg 189
Db 172 ctgttcccatgagcgggctggccaggggccaggcgctccagcccgcggtggagatg 231
QY 190 gcgttgatgatgtcaacaagcagccgaatctgtcgcgggcttcaagctcatcctgcac 249
Db 232 gcgttgaggacgtgaagccgcaggagacatcctgcggactatgagctcaagctcatc 291
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1348 aaatggattgagggtccccccagctgaccagacctggfcatcaagacattccgcttc 1407
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1408 ctgtcacagaactcttatctcgtctcagttctctcagcctgggcatgtctctagct 1467
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1864 gtatctactactatgatataaataacgtccagatctgagcatttgaaagtcaacgc 1923
1888 aaggagatatctgacg---tctctattctgccccagctggagcattgcagctccaggag 1944
1924 aactccatgtggttgggtctgtatacggcttcaagggttaactcctgtgttttgccctc 1983
1945 atgaatacatggttgccatttctatggttacaaagggtcgtcgtcgtcgtcgtggaatc 2004
1984 ttttggcgtacagacgcgtccctcattaaagtgaacagatcaacgattcgcgttatgtg 2043
2005 ttctctgttatgagaccacagagtggttccactgagaagatcaatgatcacccggctgtg 2064
2044 ggcataagcatctataacgtgggtgtccttctgtctgataacagctcccggtgggcatgtc 2103
2065 ggcattggtatctacaatgtggcagtcctgtgctcactcatcactgtcctgtcaccatgatt 2124
2104 attgcatcgcaacagagcgcgtcttctgcttctgctctagctgtgatatcttctgtgt 2163
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2284 tatcagaacttcttaccgaaaacagcaattgcaacgattataaacaagaaggaggaa 2343
2305 gagaagcccggtctgttggagaaggagaaaccgtagaactggaaaagatcattgtctgagaaa 2364
2344 aagattcagctcctgcgacagcgtc 2368
2365 gaggagcgtgtctcgaactgcgcc 2389
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RESULT 13

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AA293411
ID AA293411 standard; cDNA; 2914 BP.
XX
AC AA293411;
XX
DT 24-JUL-2000 (first entry)
XX
DE Human GABAB1A receptor coding sequence.
XX
KW GABAB1A receptor; G-protein; disease; treatment; detection;
KW therapy; antibody; immune response; infection; cancer; diabetes;
KW obesity; anorexia; bulimia; Parkinson's disease; heart failure;
KW hypotension; hypertension; urinary retention; osteoporosis;
KW angina pectoris; myocardial infarction; stroke; ulcers; asthma;
KW allergy; benign prostatic hypertrophy; migraine;
KW neurological disorders including anxiety; schizophrenia;
KW depression; dementia; Huntington's disease;
KW Gillies de la Tourette's syndrome; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
CDS 1..2883
FT /*tag= a
FT /product= GABAB1A receptor
XX
PN WO200012106-A1.
XX
PD 09-MAR-2000.
XX
PF 30-AUG-1999; 99WO-US19435.
XX
PR 01-SEP-1998; 98US-O144779.
XX
PA (SMIK ) SMITHKLINE BEECHAM CORP.
XX
PI Elshourbagy NA;
XX
DR WPI; 2000-237771/20.
XX
DR P-PSDB; AAY83145.
XX
PT New GABAB1A polypeptide useful for diagnosis, treatment and prevention
PT of diseases associated with its expression including infections,
PT psychotic and neurological disorders and cancer
XX
PS Claim 2; page 33-34; 38pp; English.
XX
CC The GABAB1A receptor is believed to be a member of the GABAB
CC family of polypeptides. They are therefore of interest because
CC members of the purinergic 7TM receptor family (G-protein coupled
CC receptors) of genes are involved in a number of biological and
CC disease manifestations. They are also a successful target for
CC pharmaceutical intervention. Antibodies directed against GABAB1A
CC and its peptides can be used to treat bacterial, fungal, protozoan
CC and viral infections, pain, cancers, diabetes, obesity, anorexia,
CC bulimia, Parkinson's disease, acute heart failure, hypotension,
CC hypertension, urinary retention, osteoporosis, angina pectoris,
CC myocardial infarction, stroke, ulcers, asthma, allergies, benign
CC prostatic hypertrophy, migraine, vomiting, psychotic and
CC neurological disorders including anxiety, schizophrenia, depression,
CC dementia and severe mental retardation and dyskinesias such as
CC Huntington's disease or Gilles de la Tourette's syndrome. The
CC GABAB1A polypeptide or a vector comprising a sequence encoding the
CC polypeptide can be used to induce an immunological response in a
CC mammal to protect against disease. The presence or absence of a
CC mutation in the nucleotide sequence encoding the GABAB1A polypeptide
CC can be detected in the genome of a subject and/or the presence or
CC amount of expression of the polypeptide in a sample from the subject
CC can be analysed and used to diagnose a disease or susceptibility to a
CC disease related to the expression or activity of GABAB1A.
CC Diagnosis can be measured at the RNA level using nucleic acid
CC amplification, e.g. polymerase chain reaction, RNase protection or
CC Northern blotting or at the protein level by radioimmunoassay,
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CC competitive-binding assays, Western blot analysis or ELISA assays
CC (enzyme linked immunosorbent assay).

XX Sequence 2914 BP; 638 A; 825 C; 816 G; 635 T; 0 other;

Query Match 22.6%; Score 569.4; DB 21; Length 2914;
Best Local Similarity 54.8%; Pred. No. 4.3e-170;
Matches 1231; Conservative 0; Mismatches 98; Indels 33; Gaps 4;

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DB 520 ctgtttcccatgagcggggctggccaggggccaggcctgcagcccggtggagatg 579
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||
QY 190 gcgttgatgatgtcaacaacagcgcgaatctgtctgcggggttcaagctcatcctgcac 249
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||
DB 580 gcgtggaggacgtgaatagccgcaggagacatcctgcgggactatgagctcaagctcatc 639
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QY 250 agcaacgacagcagtgtagcccggtttggcgccagcgtgatgtacaaatctgctctat 309
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DB 640 caccagacagaagtgtatccaggccaagcccaagtaacctatgatgctgctctac 699
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DB 700 aacgacctataagatcatcttatgccggctgcagctgtctccagctgtgtgct 759
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QY 370 gagctgcacaaatgtggaactaatgtgtctctgctacggggcctcagtcggctctt 429
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DB 760 gagctgtagatgtggaacctcaatgtcttctctatggtccagctcaccagccctg 819
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QY 490 ccaacgcgcatacagctgatgaagaaattcgctggtctccgggtggccattctcgagcag 549
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DB 940 accactgaggtctctcaactcgactctgacgacctggaggaaacgagtgaggcgtgga 999
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AUTHORS Mezler, M., Mueller, T. and Raming, K.
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RESULT 2

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LOCUS Drosophila melanogaster, *** SEQUENCING IN PROGRESS ***, in ordered
DEFINITION pieces.
ACCESSION AC019747
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AC019747 53444 bp DNA HTG 03-JAN-2000

VERSION
KEYWORDS
SOURCE
ORGANISM

AC019747.1 GI:6665150
HTG: HTCS_PHASE2.
fruit fly.

REFERENCE

Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.

AUTHORS

1 (bases 1 to 53444)
Adams, M. and Venter, J. C.

TITLE

Direct Submission
Submitted (30-DEC-1999) Celera Genomics, 45 West Gude Drive,
Rockville, MD, USA

COMMENT

This sequence was identified as CDW:10210817 by the submitter.
For more information on this record e-mail to fly@celera.com.

- * NOTE: This is a 'working draft' sequence.
- * This sequence will be replaced
- * by the finished sequence as soon as it is available and
- * the accession number will be preserved.

FEATURES

source

1. .53444
/organism="Drosophila melanogaster"
/db_xref="taxon:7227"

BASE COUNT

15987 a 10982 c 10952 g 15523 t

ORIGIN

Query Match 26.6%; Score 672; DB 2; Length 53444;

Best Local Similarity 74.9%; Pred. No. 1.6e-186;

Matches 1087; Conservative 0; Mismatches 0; Indels 365; Gaps 5;

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Holt, R.A., Evans, C.A., Gocayne, J.D., Amanatides, P.G., Brandon, R.C., Rogers, Y., An, H., Baldwin, D., Banzon, J., Beeson, K.Y., Busam, D.A., Carlson, J.W., Center, A., Champe, M., Davenport, L.B., Dietz, S.M., Dodson, K., Dorsett, V., Doup, L.E., Doyle, C., Dresnek, D., Farfan, D., Ferriera, S., Frise, E., Galle, R.F., Garg, N.S., George, R.A., Gonzalez, M., Houck, J., Hoskins, R.A., Hostin, D., Howland, T.J., Ibegwam, C., Jalali, M., Kruse, D., Li, P., Mattel, B., Moshrefi, A., McIntosh, T.C., Moy, M., Murphy, B., Nelson, C., Nelson, K.A., Nunoo, J., Paclebe, J., Paragas, V., Park, S., Patel, S., Pfeiffer, B., Phouanenavong, S., Pittman, G.S., Puri, V., Richards, S., Scheeler, F., Stapleton, M., Strong, R., Svirskas, R., Tector, C., Williams, S.M., Zaveri, J.S., Smith, H.O., Rubin, G.M. and Venter, J.C.

Sequencing of *Drosophila* chromosome 2L, region 36X-36X unpublished

2 (bases 1 to 184682)

Celniker, S.E., Adams, M.D., Krommiller, B., Tyler, D., Wan, K.H., Holt, R.A., Evans, C.A., Gocayne, J.D., Amanatides, P.G., Brandon, R.C., Rogers, Y., An, H., Baldwin, D., Banzon, J., Beeson, K.Y., Busam, D.A., Carlson, J.W., Center, A., Champe, M., Davenport, L.B., Dietz, S.M., Dodson, K., Dorsett, V., Doup, L.E., Doyle, C., Dresnek, D., Farfan, D., Ferriera, S., Frise, E., Galle, R.F., Garg, N.S., George, R.A., Gonzalez, M., Houck, J., Hoskins, R.A., Hostin, D., Howland, T.J., Ibegwam, C., Jalali, M., Kruse, D., Li, P., Mattel, B., Moshrefi, A., McIntosh, T.C., Moy, M., Murphy, B., Nelson, C., Nelson, K.A., Nunoo, J., Paclebe, J., Paragas, V., Park, S., Patel, S., Pfeiffer, B., Phouanenavong, S., Pittman, G.S., Puri, V., Richards, S., Scheeler, F., Stapleton, M., Strong, R., Svirskas, R., Tector, C., Williams, S.M., Zaveri, J.S., Smith, H.O., Rubin, G.M. and Venter, J.C.

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VERSION AE003646.2 GI:10728794
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SOURCE fruit fly.
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Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
1 (bases 1 to 266308)
AUTHORS Adams,M.D., Celniker,S.E., Holt,R.A., Evans,C.A., Gocayne,J.D.,
Amanatides,P.G., Scherer,S.E., Li,P.W., Hoskins,R.A., Galle,R.F.,
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Brandon,R.C., Rogers,Y.H., Blazer,R.G., Champe,M., Pfeiffer,B.D.,
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Benos,P.V., Berman,B.P., Bhandari,D., Bolshakov,S., Borkova,D.,
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Pollard,J., Puri,V., Reese,M.G., Reinert,K., Remington,K.,
Saunders,R.D., Scheeler,F., Shen,H., Shue,B.C., Siden-Kiamos,I.,
Simpson,M., Skupski,M.P., Smith,T., Spier,E., Spradling,A.C.,
Stapleton,M., Strong,R., Sun,E., Svirska,R., Tector,C., Turner,R.,
Venter,E., Wang,A.H., Wang,X., Wang,Z.Y., Wassarman,D.A.,
Weinstock,G.M., Weissbach,J., Williams,S.M., Woodage,T.,
Worley,K.C., Wu,D., Yang,S., Yao,Q.A., Ye,J., Yeh,R.F.,
Zaveri,J.S., Zhan,M., Zhang,G., Zhao,Q., Zheng,L., Zheng,X.H.,
Zhong,F.N., Zhong,W., Zhou,X., Zhu,S., Zhu,X., Smith,H.O.,
Gibbs,R.A., Myers,E.W., Rubin,G.M. and Venter,J.C.
The genome sequence of Drosophila melanogaster
Science 287 (5461), 2185-2195 (2000)
JOURNAL 20196006
MEDLINE 2 (bases 1 to 266308)
REFERENCE 2 (bases 1 to 266308)
AUTHORS Adams,M.D., Celniker,S.E., Gibbs,R.A., Rubin,G.M. and Venter,C.J.

TITLE Direct Submission
JOURNAL Submitted (21-MAR-2000) Celera Genomics, 45 West Gude Drive,
Rockville, MD, USA
COMMENT On Oct 9, 2000 this sequence version replaced gi:7298191.
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ORGANISM	Drosophila melanogaster			
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TITLE	An exploration of the sequence of a 2.9-Mb region of the genome of Drosophila melanogaster: the Adh region			
JOURNAL	Genetics 153 (1), 179-219 (1999)			
MEDLINE	99403001			

PUBMED
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2 (bases 1 to 303043)
Celnikier S.E., Agbayani, A., Arcaina, T.T., Baxter, E., Blazej, R.G.,
Butenhoff, C.M., Champe, M., Chavez, C., Chew, M., Ciesielska, L.,
Doyle, C.M., Farfan, D.E., Galle, R., George, R.A., Harris, N.L.,
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Rubin, G.M.

TITLE
JOURNAL

Direct Submission
Submitted (08-MAR-2000) Berkeley Drosophila Genome Project,
Lawrence Berkeley National Laboratory, MS 64-121, Berkeley, CA
94720, USA

COMMENT

On Mar 22, 2000 this sequence version replaced gi:1103948
gi:2337899 gi:1945594 gi:2337902 gi:2335080 gi:2920814 gi:2342705.
Submitted by the Berkeley Drosophila Genome Project. For more
information, visit the BDGP Web site: <http://www.fruitfly.org/> This
is the finished sequence of 34C4-36A7.

The orientation of this sequence along the chromosome is left to
right. This sequence was annotated by Sima Misra
(sima@fruitfly.berkeley.edu) on behalf of the Berkeley Drosophila
Genome Center. Coding sequences are predicted based on
computational analysis, using both gene and CDS prediction programs
and matches to other sequences. These predictions and matches have
been evaluated by the annotators and may have been refined by hand.
The annotators have also used their judgement about which matches
to include in this record. The annotations on this sequence can be
examined in more detail from
<http://www.fruitfly.org/publications/Adh.html>
The annotation syntax used in this record is documented at
ftp://ftp.ebi.ac.uk/pub/databases/edgp/sequence_annotation.README.v1.2.

FEATURES
source

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ACCESSION AX054691
VERSION AX054691.1 GI:12228215
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REFERENCE 1 (bases 1 to 2886)
AUTHORS Ng, G. and O'Neill, G.
TITLE Use of gabapentin in assays to identify gabab receptor modulators
JOURNAL Patent: WO 0073788-A 23 07-DEC-2000;
Merck Frost Canada & Co. (CA)
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VERSION	AJ012186.1	GI:3776093	
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ORGANISM	Homo sapiens		
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AUTHORS	White, J. H., Wise, A., Main, M. J., Green, A., Fraser, N. J., Disney, G. H., Barnes, A. A., Emson, P., Foord, S. M. and Marshall, F. H.		
TITLE	Heterodimerization is required for the formation of a functional GABA(B) receptor		
JOURNAL	Nature	396 (6712), 679-682	(1998)
MEDLINE	99087321		
REFERENCE	2	(bases 1 to 2535)	
AUTHORS	Fraser, N. J.		
TITLE	Direct Submission		
JOURNAL	Submitted (16-OCT-1998)	Fraser N. J., Receptor Systems, Cellular Sciences, Glaxowellcome, Medicines Research Centre, Gunnels Wood Road, Stevenage, Herts. SG1 2NY, U.K	
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LOCUS HSA012187 2700 bp mRNA PRI 24-APR-1999
DEFINITION Homo sapiens mRNA for GABAB receptor, subunit 1c..
ACCESSION AJ012187
VERSION AJ012187.1 GI:3776095
KEYWORDS GABAB receptor; gabab-R1 gene; Subunit 1c.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 2700)
AUTHORS Fraser, N.J.
TITLE Direct Submission
JOURNAL Submitted (16-Oct-1998) Fraser N.J., Receptor Systems, Cellular
Sciences, GlaxoWellcome, Medicines Research Centre, Gunnels Wood
Road, Stevenage, Herts. SG1 2NY, U.K.
FEATURES
Location/Qualifiers
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BASE COUNT 599 a 764 c 740 g 597 t
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Query Match 22.6%; Score 569.4; DB 9; Length 2700;
Best Local Similarity 54.8%; Pred. No. 2e-156;
Matches 1231; Conservative 0; Mismatches 981; Indels 33; Gaps 4;
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Db	1639	TACAAGAAGATTGGCTACTACTGACAGCACCAAGGATGATCTTCTCTGGTCCAAAACAGAT	1698
Qy	1330	cagtggaatggttggeaagtttoctcaagatcgocacaattgtcaacccatgttctacgcacc	1389
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Qy	1510	ccggttgcaatacagatcatgttatcttggtgtcatcatctgttotaataatctgtcatcttta	1569
Db	1879	CCCAACCTGAACAACTGACTGCTGTGGCTGTCTACTTGGCTTTAGCTGTCTTCTCC	1938
Qy	1570	ctgggcacgcagcgagcgtttgtcagcccgaggaaatataccaaagatatgtcaagcgcg	1629
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Qy	1690	cgtgtgcatacgtttttacaacaa-----aagcaaaactgacccaaagaaaaaagtggaa	1743
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Db	2296	ATGAATACATGGCTTTGGCATTTTCTATGGTTTACAAGGGGCTGCTGCTGTCTGGGAATC	2355
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Qy	2284	tatcagaacttgttaccgaaacagcaaatctgcaacgattataatacaacagaggaggaa	2343
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LOCUS			PRI
DEFINITION		Homo sapiens mRNA for GABA-B Rlb receptor.	11-DEC-1998
ACCESSION		AJ225029	
VERSION		AJ225029.1	GI:3892873
KEYWORDS		GABA-B receptor.	
SOURCE		human.	
ORGANISM		Homo sapiens	
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AUTHORS		Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	
TITLE		1 (bases 1 to 2928)	
JOURNAL		Kaupmann K., TA Nervous System, Novartis	
PHARMACEUTICAL		Pharma AG, K-125.6.20, CH-4002 Basel, SWITZERLAND	
REFERENCE		2 (bases 1 to 2928)	
AUTHORS		Kaupmann,K., Schuler,V., Mosbacher,J., Bischoff,S., Bittiger,H., Heid,J., Froestl,W., Leonhard,S., Praeff,T., Karschin,A. and Bettler,B.	
TITLE		Human gamma-aminobutyric acid type B receptors are differentially expressed and regulate inwardly rectifying K+ channels	
JOURNAL		Proc. Natl. Acad. Sci. U.S.A. 95 (25), 14991-14996 (1998)	
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Query Match		22.6%	Score 569.4; DB 9; Length 2928;
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ACCESSION AF099148
VERSION AF099148.1 GI:4063891
KEYWORDS
SOURCE human.
ORGANISM
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 3192)
Stropp, U. and Raming, K.
Human mRNA for GABA-B1a receptor
JOURNAL Unpublished
REFERENCE
2 (bases 1 to 3192)
Stropp, U. and Raming, K.
Direct Submission
JOURNAL Submitted (16-OCT-1998) Central Research, Bayer AG, Leverkusen
51368, Germany
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RESULT 13

HSA225028

LOCUS HSA225028 4445 bp mRNA

DEFINITION Homo sapiens mRNA for GABA-B 1a receptor.

ACCESSION AJ225028

VERSION AJ225028.1 GI:3892593

KEYWORDS GABA-B receptor.

SOURCE human.

ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

PRI 11-DEC-1998


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REFERENCE 1 (bases 1 to 4445)
AUTHORS   Kaupmann,K.
TITLE     Direct Submission
JOURNAL   Submitted (12-MAR-1998) Kaupmann K., TA Nervous System, Novartis
          Pharma AG, K-125.6.20, CH-4002 Basel, SWITZERLAND

REFERENCE 2 (bases 1 to 4445)
AUTHORS   Kaupmann,K., Schuler,V., Mosbacher,J., Bischoff,S., Bittiger,H.,
          Heid,J., Froestl,W., Leonhard,S., Pfaff,T., Karschin,A. and
          Bettler,B.
TITLE     Human gamma-aminobutyric acid type B receptors are differentially
          expressed and regulate inwardly rectifying K+ channels
JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 95 (25), 14991-14996 (1998)
MEDLINE   99061981
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LOCUS Homo sapiens mRNA for GABA-BR1a (hGB1a) receptor.
ACCESSION Y11044
VERSION Y11044.1 GI:2826760
KEYWORDS GABA-B receptor.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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REFERENCE

1 (bases 1 to 4220)

AUTHORS

Grifa,A., Totaro,A., Rommens,J.M., Carella,M., Roetto,A., Borgato,L., Zeilante,L. and Gasparini,P.

TITLE

GABA (gamma-amino-butyric acid) neurotransmission: identification and fine mapping of the human GABAB receptor gene

JOURNAL

Biochem. Biophys. Res. Commun. 250 (2), 240-245 (1998)

MEDLINE

98440782

REFERENCE

2 (bases 1 to 4220)

AUTHORS

Gasparini,P.

TITLE

Direct Submission

JOURNAL

Submitted (04-FEB-1997) P. Gasparini, Servizio de Genetica Medica - IRCS, 'Ospedale CSS', Via Cappuccini, 71013 S Giovanni, Rotondo (FG), ITALY

REMARK

revised by submitter 28-JAN-98

COMMENT

On Jan 31, 1998 this sequence version replaced gi:2370108.

FEATURES

Location/Qualifiers

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Best Local Similarity 54.7%; Pred. No. 1.3e-155;
Matches 1229; Conservative 0; Mismatches 983; Indels 33; Gaps 4;
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QY	850	gaacagatcgaaatagctgccgaaggaacatcttgacaacggaagcgtctatgttgaatcag	909	
DB	886	GAAGAGATGACTGAGCGGTGGAGGCCATATCACCACGGAGATGTGTCTGCTGAAACCT	945	
QY	910	aaacaatcagaacaactatccggaaagactgcagaggaatttcgacatgcactgcaatcag	969	
DB	946	GCCACACCCGGAACATTTCCAACTGACATCACAGGAATTTGTGGAGAAACTAACCAAG	1005	
QY	970	gcgctaactcagagaggttacacataaccacgatacgctatccgaggggatacaggag	1029	
DB	1006	CGGCTGAAAAGACACCTGAGGAGA-----CTGGAGGCTTCCAGGAG	1047	
QY	1030	gcgcactgcctcagatgcagtgtagtggtgcttggctttcaacaagaccatggaa	1089	
DB	1048	GACCACTGCGCTATGATGCTATCTGGGCTTGGCTTTGGCCCTTGAACAAGACCTCTGGA	1107	
QY	1090	cgatgacaacccgggaagaactctcagggattttacatatacgcgaagagattgccc	1149	
DB	1108	GGAGGTGGCGGTTTCAGGAGTGGCGCTTGAGGACTTTAACTTACAACAACCCAGACATACA	1167	
QY	1150	gatgaatctagctgccatgaactccacaaattctcgggtgatatcggttgg19gga	1209	
DB	1168	GACCAAACTACCGGCCCATGAACCTCTCTCTTTGAGGGTGTCTTGGCCACGTTGTC	1227	
QY	1210	ttcagttctcagggcgatgctatgctcttcacacagatcgaaacagatgacagcgcag	1269	
DB	1228	TTTGATGCCAGCGGCTCCCGGATGGGATGGAGCTTATCGAGCAGCTACAGGCGCGCAGC	1287	
QY	1270	tacgagaagtgggttactacatactcagttggaataacctatcctggttgaatactgaa	1329	
DB	1288	TACAAGAAGATCGCTACTACGACAGCACAAGATGATCTTTCTCGTGGTCCAAAACAGAC	1347	
QY	1330	caatggattggtagaaggttctcgaatgcacaaatgtgcacccatgtctcagcaac	1389	
DB	1348	AAAGTGATCGGAGGGTCTCCCGCAGCCAGACCTTGGTTCATCAAGACATTTCCGTTTC	1407	
QY	1390	gtgtcttccattattgtgtgcatgtgcacaataatcaccagttgtggtcattcgttgc	1449	
DB	1408	CTGTACACAAACTCTTATCTCCGCTCAGTTCTCTCCAGCCTGGGCATTTGCTTGTCT	1467	
QY	1450	ttgccttgatcatctttaatatatggaataagcatagaaagatatacaaatcctcgcat	1509	
DB	1468	GTTGTCTGTCTGTCTTAACTCTACAACTCCACGTTCTGTTATATCCAGAACTCCAG	1527	
QY	1510	cccgttgcaatcagcatcatgtattgtgtgcatcatctgtctataatctgtcatctta	1569	
DB	1528	CCCAACCTCAAACTGACTGCTGTGGGCTGCTCACTGGCAGTACTGCTGTTCCCTCCC	1587	
QY	1570	ctggcgatcgagcgcgtttgtcagccccgaggaataatccaaagatatgtcaagcgcgg	1629	
DB	1588	CTTGGCTGGATGGTTACACATAGGAGAGAGCCAGTTCCTCATTTGCTGCCAGGCCCG	1647	
QY	1630	gcttggttactatccaccgggtttacactagcatcaggtgctatgttcagcaaggtctg	1689	
DB	1648	CTTTGGCTTTGGGCTTAGGCTTTAGTCTGGGCTATGGCTCTTATGTTACCAAGATCTGG	1707	
QY	1690	cgtgtgcatcgttttacaacaaaa-----gcaaaactgaccccaaaaaaagtggaa	1743	
DB	1708	TGGGTCCACACAGCTCTTCACAAAGAGAGGAGAGAGAAAGAAATGAGAGAACCTTAGAG	1767	
QY	1744	ccttggaactatacaccatggttctcgggctattatcatcatagatttaagtattactc	1803	
DB	1768	CCTTGGAAACTGTACGCCACTGTAGGCTGTGGGTGGGCATGGATATCTGACTCTGGC	1827	
QY	1804	tcattggcagatcttgcgtcgagcgttatctctgaaacattcccaactcgaagatcca	1863	

Db	1828	ATCTGGCAGATTGTGGACCCCTTGACCGAACCATTTGAGACTTTTGGCAAGGAGGAACCA	1887
Qy	1864	gtatctactactgataataaaatacgtccagagctgagcattgtgaagagtaacgc	1923
Db	1888	AAGGAGACATTGATG---TTCCTCATCTGCCCCAGCTGGAGACATGCGAGTCCCAAGAAG	1944
Qy	1924	aactccatgtggttggtctgtatcacggcttcaaggggctaatccctggtgtgttggcctc	1983
Db	1945	ATGAATACATGGCTCGGCATTTTCTATGGTTACAAGGGCTGCTGCTGCTGGGAATC	2004
Qy	1984	tttttggcgtacgacgcgcgtccattaaagtgaacacagatcaacgattcgcggttatgtg	2043
Db	2005	TTTCTTGCTTATGAGACCAAAAGTGTGTCCATGAAAAAGATCAATGACCACAGGGCCGTG	2064
Qy	2044	ggcatgacatctataacgctggctccttttgcctgataaacagctccggtgggcattggtc	2103
Db	2065	GGCATGGTCTATTACAATGTTCCGGTCTGTGCTCTCATTTACCGCTCCTGCTCACCATGATC	2124
Qy	2104	attgcatcgcaacagacgcgctcctttgccttcggttgcctcagctgtgatatctcttgtt	2163
Db	2125	CTTTCCAGCCAGCAGGAGCGACCCTTGCGCTTTGGCTCTCTGGCCATTGTTCTCTTCC	2184
Qy	2164	tctctaagcatgctgctgatattgtgcgaaggctcattgaggttatacgtcatcccaag	2223
Db	2185	TACATTACTCTGTGTTGTCTCTTTTGCTTAAGATGCGCAGGTTGTATCACTCGAGGTGAA	2244
Qy	2224	gataaggccgaatcgaaatac-----aatcccgattcagccatatcgaagaggacgaa	2277
Db	2245	TGGCAGTCTGAAGCACAGGACACATGAANAACAGGATCATCCACCACACACATGAGGAA	2304
Qy	2278	gaacgctatcagaaaacttgttaccgaaacagcaattgcaacgattataacacacaag	2337
Db	2305	GAGAAGTCCCACACTGTTGAGAAGGAACACCGTGAATTGGAAGAAGATCATCGCCGAGAA	2364
Qy	2338	gaggaagaagattcagagctcgcagacgctcgtggtggagcgg	2379
Db	2365	GAGGACGCTGTCTCTGAACCTGGCCATCGCCATCAGCTCCAGTCTCGG	2406

Search completed: May 1, 2002, 04:41:10
Job time: 10815 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: April 30, 2002, 10:12:33 ; Search time 32.13 Seconds
(without alignments)
3824.113 Million cell updates/sec

Title: US-09-715-962-2
Perfect score: 4374
Sequence: 1 MRKDMTSDGAVTFWIFLLCL.....LINSAAHATPAATLAIOTGE 840

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 473505 seqs, 146272329 residues
Total number of hits satisfying chosen parameters: 473505

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

- Database : SPTREMBL17.*
- 1: sp_archaea.*
 - 2: sp_bacteria.*
 - 3: sp_fungi.*
 - 4: sp_human.*
 - 5: sp_invertebrate.*
 - 6: sp_mammal.*
 - 7: sp_mhc.*
 - 8: sp_organelle.*
 - 9: sp_phase.*
 - 10: sp_plant.*
 - 11: sp_rodent.*
 - 12: sp_virus.*
 - 13: sp_vertebrate.*
 - 14: sp_unclassified.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	4374	100.0	840	5 Q9BML7	Q9bml7 drosophila
2	3317	75.8	1713	5 Q9V3Q9	Q9v3q9 drosophila
3	1746.5	39.9	816	5 Q9N502	Q9n502 caenorhabdi
4	1186.5	27.1	1220	5 Q9BML6	Q9bml6 drosophila
5	1183.5	27.1	1221	5 Q9Y133	Q9y133 drosophila
6	1022.5	23.4	1305	5 Q9VPS7	Q9vps7 drosophila
7	1018.5	23.3	1305	5 Q9BML5	Q9bml5 drosophila
8	457	10.4	402	5 Q23442	Q23442 caenorhabdi
9	362.5	8.3	976	5 Q9V485	Q9v485 drosophila
10	343.5	7.9	983	11 Q62916	Q62916 rattus norv
11	342	7.8	879	11 Q9QYS2	Q9qys2 mus musculus
12	334.5	7.6	528	5 Q96954	Q96954 geodia cydo
13	330	7.5	872	4 Q9H3N6	Q9h3n6 homo sapien
14	330	7.5	977	13 Q9PWEL	Q9pwe1 ictalurus p
15	299.5	6.8	1188	13 Q9BUC5	Q9buc5 gallus gall
16	297.5	6.8	1242	13 Q9BUC4	Q9buc4 gallus gall
17	294.5	6.7	1156	13 Q9BUC6	Q9buc6 gallus gall
18	274.5	6.3	153	11 Q9QY85	Q9qy85 rattus norv
19	267	6.1	1199	11 Q9EPV6	Q9epv6 mus musculus

20	247.5	5.7	870	5	Q9N4T8	Q9n4t8 caenorhabdi
21	243.5	5.6	856	13	Q73638	Q73638 fugu rubrip
22	241.5	5.5	868	13	Q73636	Q73636 fugu rubrip
23	240	5.5	912	10	Q9C561	Q9c561 arabidopsis
24	237	5.4	877	13	Q9PW88	Q9pw88 carassius a
25	235	5.4	844	13	Q93552	Q93552 carassius a
26	231.5	5.3	738	5	Q9V4U3	Q9v4u3 drosophila
27	231.5	5.3	864	13	Q73637	Q73637 fugu rubrip
28	227	5.2	875	13	Q73640	Q73640 fugu rubrip
29	224.5	5.1	1056	13	Q9Y117	Q9y117 squalus aca
30	223	5.1	1055	13	Q9YGW3	Q9ygw3 oryzias lat
31	222	5.1	1055	13	Q98U11	Q98u11 oryzias lat
32	219.5	5.0	848	13	Q93553	Q93553 carassius a
33	219	5.0	941	10	Q9SWD9	Q9swd9 arabidopsis
34	212	4.8	1267	5	Q93564	Q93564 caenorhabdi
35	211.5	4.8	925	10	Q65498	Q65498 arabidopsis
36	211.5	4.8	962	10	Q23048	Q23048 arabidopsis
37	209	4.8	1070	13	Q93490	Q93490 anguilla ja
38	207	4.7	808	11	Q35190	Q35190 mus musculu
39	202.5	4.6	880	13	Q73639	Q73639 fugu rubrip
40	201.5	4.6	912	10	Q9SES5	Q9ses5 brassica na
41	195	4.5	843	11	Q9Z0R7	Q9z0r7 rattus norv
42	193.5	4.4	551	13	Q9PWQ0	Q9pwq0 fugu rubrip
43	190.5	4.4	923	10	Q9ZV68	Q9zv68 arabidopsis
44	189.5	4.3	953	10	Q9ZV67	Q9zv67 arabidopsis
45	187	4.3	502	13	Q98845	Q98845 anguilla ja

ALIGNMENTS

RESULT 1

Q9BML7	PRELIMINARY;	PRT;	840 AA.
ID	Q9BML7		
AC	Q9BML7;		
DT	01-JUN-2001 (TREMBLrel. 17, Created)		
DT	01-JUN-2001 (TREMBLrel. 17, Last sequence update)		
DE	01-JUN-2001 (TREMBLrel. 17, Last annotation update)		
DE	METABOTROPIC GABA-B RECEPTOR SUBTYPE 1.		
GN	GABA-B-R1.		
OS	Drosophila melanogaster (Fruit fly).		
OC	Eukaryota; Metazoa; Arthropoda; Insecta; Hexapoda; Insecta;		
OC	Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;		
OC	Ephydroidea; Drosophilidae; Drosophila.		
OX	NCBI_TaxID=7227;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RX	PubMed-11168554;		
RA	Mezler M., Muller T., Raming K.;		
RT	*Cloning and functional expression of GABA-B receptors from		
RL	Drosophila.*;		
RL	Eur. J. Neurosci. 13:477-486(2001).		
DR	EMBL; AF318272; AAK13420.1; -		
KW	Receptor.		
SQ	SEQUENCE 840 AA; 94384 MW; C09LA9F406C97500 CRC64;		

Query Match	100.0%;	Score 4374;	DB 5;	Length 840;
Best Local Similarity	100.0%;	Pred. No. 0;		
Matches 840;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
Qy	1	MRKDMTSDGAVTFWIFLLCLIASPHLQGVAGRPDELHIGGIFFIAGKGGWGGQACMPA 60		
Db	1	MRKDMTSDGAVTFWIFLLCLIASPHLQGVAGRPDELHIGGIFFIAGKGGWGGQACMPA 60		
Qy	61	TRLALDDVKNQPNLPGPKLILHSNDSECEPGISAVMYNLLYNKPKMLLLAGCSTVCT 120		
Db	61	TRLALDDVKNQPNLPGPKLILHSNDSECEPGISAVMYNLLYNKPKMLLLAGCSTVCT 120		
Qy	121	TVAAAKMWNILVLCYGASSPALSDDRKFPLFRTHPSATVHNPTRIKLMKFFGHSRAV 180		
Db	121	TVAAAKMWNILVLCYGASSPALSDDRKFPLFRTHPSATVHNPTRIKLMKFFGHSRAV 180		

QY 181 LOAAEEVISTVEDLENRCMEAGVEIVTROSFLSDPTDAVNLRRDARIIVGLFYVAA 240
Db 181 LOAAEEVISTVEDLENRCMEAGVEIVTROSFLSDPTDAVNLRRDARIIVGLFYVAA 240
QY 241 RRVLCEMYKOOLYGRAHVWFIFIGWYEDNWYEVNLKABGICTCTVQBMRIAABGHLTTEALM 300
Db 241 RRVLCEMYKOOLYGRAHVWFIFIGWYEDNWYEVNLKABGICTCTVQBMRIAABGHLTTEALM 300
QY 301 WNONNOTTISGMTAEERHRLNQAALIEEGYDINHDIRYPEGVQEAFLAYDAVWSVALAFNK 360
Db 301 WNONNOTTISGMTAEERHRLNQAALIEEGYDINHDIRYPEGVQEAFLAYDAVWSVALAFNK 360
QY 361 TMRLLTGGKSLRDFYVTDKEIDAIEIYAAMNSTQFLGSGVVAFFSSOGDRIALTOIEQMI 420
Db 361 TMRLLTGGKSLRDFYVTDKEIDAIEIYAAMNSTQFLGSGVVAFFSSOGDRIALTOIEQMI 420
QY 421 DGYEKELGYDITQDNLNLSWLTQEWIGKVPQDRTIYTHVLRVTSVLPFLVCMCTISSCGI 480
Db 421 DGYEKELGYDITQDNLNLSWLTQEWIGKVPQDRTIYTHVLRVTSVLPFLVCMCTISSCGI 480
QY 481 FVAFALIIFNIWKNHRRVIOSSHPCVNTIMLFGVILCLISVILLIDGRFVSPPEYPRIC 540
Db 481 FVAFALIIFNIWKNHRRVIOSSHPCVNTIMLFGVILCLISVILLIDGRFVSPPEYPRIC 540
QY 541 QARAWLLSTGFTLAYGAMFSKVRVHRFTTKAKTDPKKVPKWLKTYMTWSGLLSIDLVL 600
Db 541 QARAWLLSTGFTLAYGAMFSKVRVHRFTTKAKTDPKKVPKWLKTYMTWSGLLSIDLVL 600
QY 601 LSWQIFDPLQRYLETPLDPVSTDDIKIRPELEHESORNWMLGLVYFGKLLVFG 660
Db 601 LSWQIFDPLQRYLETPLDPVSTDDIKIRPELEHESORNWMLGLVYFGKLLVFG 660
QY 661 LFLAYETRSIKVQINDSRVVGMSIYNNVVLCLITAPVGMVIAISOQDASFVALAVIFC 720
Db 661 LFLAYETRSIKVQINDSRVVGMSIYNNVVLCLITAPVGMVIAISOQDASFVALAVIFC 720
QY 721 CFTSMILLIFVPKVIETIRHPKDAESKYNPDSSAISKEDEERYQKLVTEQOLRLITQKE 780
Db 721 CFTSMILLIFVPKVIETIRHPKDAESKYNPDSSAISKEDEERYQKLVTEQOLRLITQKE 780
QY 781 EKIRLVRORLVERGDAGTELNGATGASAAVATTSOPASLINSNAHATPAATLAIQGE 840
Db 781 EKIRLVRORLVERGDAGTELNGATGASAAVATTSOPASLINSNAHATPAATLAIQGE 840

RESULT 2
Q9V309 PRELIMINARY; PRT: 1713 AA.
ID Q9V309
AC Q9V309
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE CG15274 PROTEIN
GN GABA-B-R1 OR EG:DS00929.6 OR CG15274.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
[1]
RP SEQUENCE FROM N.A.
RN STRAIN=BERKELEY;
RC MEDLINE=20196006; PubMed=107311132;
RX Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scher S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA Sutton G.G., Wortman J.R., Vandeil M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkuch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Bertram B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,

RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K.J., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Foster C., Gabrielian A.E., Garg N.S., Galbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam K.A.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattel B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Mishina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wassarman D.A., Weinstein G.M., Weissbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster.";
RL Science 287:2185-2195(2000).
[2]
RN SEQUENCE FROM N.A.
RP STRAIN=Y, AND CN BW SP;
RC MEDLINE=99403001; PubMed=10471707;
RX Ashburner M., Misra S., Roote J., Lewis S.E., Blazej R., Davis T.,
RA Doyle C., Galle R., George R., Harris N., Hartzell G., Harvey D.,
RA Hong L., Houston K., Hoskins R., Johnson G., Martin C., Moshrefi A.,
RA Palazzolo M., Reese M.G., Spradling A., Tsang G., Wan K., Whitelaw K.,
RA Celniker S., Rubin G.M.;
RT "An exploration of the sequence of a 2.9-Mb region of the genome of
Drosophila melanogaster: the Adh region.";
RL Genetics 153:179-219(1999).
[3]
RN SEQUENCE FROM N.A.
RP STRAIN=Y, AND CN BW SP;
RC Celniker S.E., Agbayani A., Arcaina T.T., Baxter E., Blazej R.G.,
RA Butenhoff C., Champe M., Chavez C., Chew M., Ciesiolka L., Doyle C.M.,
RA Farfan D.E., Galle R., George R.A., Harris N.L., Hoskins R.A.,
RA Houston K.A., Hummasti S.R., Karra K., Kearney L., Kim E., Lee B.,
RA Lewis S., Li P., Lomotan M.A., Mazda P., Moshrefi A.R., Moshrefi M.,
RA Nixon K., Pacleb J.M., Park S., Pfeiffer B., Poon L., Sequeira A.,
RA Sethi H., Snir E., Svirskas R.R., Wan K.H., Weinburg T., Zhang R.,
RA Zieran L.L., Rubin G.M.;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AE003646; AAF53431.1; -;
DR EMBL; AE003411; AAF4910.1; -;
DR FlyBase; FBgn0028924; GABA-B-R1.
DR InterPro; IPR001828; ANF_receptor.
DR InterPro; IPR000337; GPCR_Mgr.
DR InterPro; IPR000402; Na_K_beta.
DR Pfam; PF00003; 7cm_3; 1.
DR Pfam; PF01094; ANF_receptor; 1.
DR Pfam; PF00287; Na_K-ATPase; 1.
DR PROSITE; PS0259; G_PROTEIN_RECEP_F3_4; 2.
KW Hypothetical protein.
SQ SEQUENCE 1713 AA; 195133 MW; 8474EBC5F9FA27AC CRC64;

Query Match 75.8%; Score 3317; DB 5; Length 1713;
Best Local Similarity 45.0%; Pred. No. 7.3e-251;
Matches 737; Conservative 16; Mismatches 19; Indels 866; Gaps 10;
Qy 3 KDMTSDGAVTFWIFLLCLITASPHLOGVAGRDELHIGGIFTAGKGGWGGACMPATR 62
Db 142 RDMTSDGAVTFWIFLLCLITASPHLOGVAGRDELHIGGIFTAGKGGWGGACMPATR 201

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Qy 63 LALDDVNKOPNLLPGFKLILHSNDSECEPGLGASVMYNLLYNKPKMLLAGCSTVCTTV 122
Db 202 LALDDVNKOPNLLPGFKLILHSNDSECEPGLGASVMYNLLYNKPKMLLAGCSTVCTTV 261
Qy 123 AEAAMWNLIVLCYGASSPALSDRRFPFLFRTHPSATVHNPTRIKLMKKFGHSRVAILQ 182
Db 262 AEAAMWNLIVLCYGASSPALSDRRFPFLFRTHPSATVHNPTRIKLMKKFGHSRVAILQ 321
Qy 183 QAEVFI STVELENRCMEAGVEI VTROSFLSDPTDAVNLRRQDARIIVGLFVVAARR 242
Db 322 QAEVFI STVELENRCMEAGVEI VTROSFLSDPTDAVNLRRQDARIIVGLFVVAARR 381
Qy 243 VLEMYKQOLYGRAHWFFIGHYEDNWVEYNLKAEGITCTVEQMRTAAEGHLLTEALMWN 302
Db 382 VLEMYKQOLYGRAHWFFIGHYEDNWVEYNLKAEGITCTVEQMRTAAEGHLLTEALMWN 441
Qy 303 QNNQTTISGMTAEERF-----RHRLNOALIEEGYDINHDRYPEGY 341
Db 442 QNNQTTISGMTAEERFVLVLLYPLKFLLOCAFFLRHRLNOALIEEGYDINHDRYPEGY 501
Qy 342 QEAPLAYDAVMSVALAFNKMTMERLTGTGKSLRDFYTDKEIADEIYAAMNSTOFLGVSQV 401
Db 502 QEAPLAYDAVMSVALAFNKMTMERLTGTGKSLRDFYTDKEIADEIYAAMNSTOFLGVSQV 561
Qy 402 VAFSSQGDRIALTOEQMIDGKYEKLYGYDTQDNLNLSWNTQWIGGK-----449
Db 562 VAFSSQGDRIALTOEQMIDGKYEKLYGYDTQDNLNLSWNTQWIGGKTKHVTTEPNKN 621
Qy 450 -----449
Db 622 GNPSSKDDVNTGRSLTSLSEKNDENKPNSSASLOQAPKVPKPKLSISDAGKDTVTQKV 681
Qy 450 -----449
Db 682 KENBEPGSKOFKESIGVRANRNSATKKENEKLLVKTVPCKSLIKESNDENVEPSRRT 741
Qy 450 -----449
Db 742 KSQPVGKKVYBESSTRVREPDPDFDREKLYSDMIDYDRSSDVPKPKLSWEPDSTLRRR 801
Qy 450 -----VQO-----452
Db 802 FVSNNEXHSSLEGEDEEIDLDSVGSSTMRGYSYRMPQNAEDERPVLIAETINMGKELKE 861
Qy 453 -----DRTI-----LRTVSLPLFV-----460
Db 862 QRESTNVPNRNRDRTIDEVKGKITGTSKQHVVEKYNETASNEDDDNAQVKHGTIT 921
Qy 461 -----460
Db 922 KIFSTIAORMKEKSKSEEDENKDNKDKKDDQKLPPEPEIELEAKKAWTFPI 981
Qy 461 -----460
Db 982 AETSPDIPGENQILQYOKVKIGKRNRYRCIGINTDISRKSKITFISKSAGDDLWVYH 1041
Qy 461 -----LRTVSLPLFV-----470
Db 1042 DGGRLRDIGQTTENLKNRKNHKKHTEPDDIPVDIGHSDDRVREIGVNTKLPKLIIPPI 1101
Qy 471 -----470
Db 1102 AEMHVHKNGLRDICTSTDKPWPIDGTDVLYMHPKTDKRLKLNKLIYDPPDNGPYKM 1161
Qy 471 -----C-----MCTISCGIFVAFALII 488
Db 1162 PTKEDRRTYYKGEYHFPGRTWRRLFENKIHGKYKLRPSHWLVTLVFSLVILFVIIF 1221
Qy 489 FNW-----492
Db 1222 SWAFWDFIKDDASRKVPIMKKAQPFISFTPIGPRTPNKAVSFDPNRNSTEVMKYAGINAL 1281
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Qy 493 -----492
Db 1282 LEKYGDYGHNPFRFCTCTANERKFGYPSGEPVFLKVNRIIGFKTEPYINSDELVRKIDEV 1341
Qy 493 -----N 493
Db 1342 EFTALKRLLENTTTEEGHLNRTWITCRSDKDKNVLIIEPHPEPAIRTEYTDIEEKIEYIAN 1401
Qy 494 KHRR-----VIOSSHPVCNTIMLFGVITCLISVI 522
Db 1402 EGKKSFFGPNVNRIVALKIKNLKANERVHINCKTIVIOSSHPVCNTIMLFGVITCLISVI 1461
Qy 523 LLGIDGRFVSPPEYPKICOARAWLLSTGFTLAYGAMFSKVVRHRTTKAKTDPKKKVEP 582
Db 1462 LLGIDGRFVSPPEYPK-----1477
Qy 583 WKLYTWVSGLLSIDLVILLSSQIIFDPLQRYLETPLFDPVSTTDDIKIRPELEHESORN 642
Db 1478 -----IFDPLQRYLETPLFDPVSTTDDIKIRPELEHESORN 1515
Qy 643 SMWGLVYGFKGLILVFLGLFLAYETRSIKVKOINDSRVYVMSIYVNVVLCITAPVGMVI 702
Db 1516 SMWGLVYGFKGLILVFLGLFLAYETRSIKVKOINDSRVYVMSIYVNVVLCITAPVGMVI 1575
Qy 703 ASQODASFAFVALAVIFCCFLSMILLIFVPKVIIEVIRHPKDKAESKYNPDSAISKEDEERY 762
Db 1576 ASQODASFAFVALAVIFCCFLSMILLIFVPKVIIEVIRHPKDKAESKYNPDSAISKEDEERY 1635
Qy 763 QKLVTENEOQLRLTOKEEKIRVLRORLVERGDAGKTELNGATGVASAAVATTQSPASLI 822
Db 1636 QKLVTENEOQLRLTOKEEKIRVLRORLVERGDAGKTELNGATGVASAAVATTQSPASLI 1695
Qy 823 NSSAHATPAATLAIQTGE 840
Db 1696 NSSAHATPAATLAIQTGE 1713
RESULT 3
Q9N502 PRELIMINARY; PRT; 816 AA.
AC Q9N502;
DT 01-OCT-2000 (Tremblrel. 15, Created)
DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)
DT 01-JUN-2001 (Tremblrel. 17, Last annotation update)
DE Y41G9A.4 PROTEIN.
GN Y41G9A.4
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidae;
OC Rhabditidae; Peloderinae; Caenorhabditis.
RN NCBI_TaxID=6239;
RX [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BRISTOL N2;
RX MEDLINE=99069613; PubMed=9851916;
RA None;
RT "Genome sequence of the nematode C. elegans: a platform for
RL Science 282:2012-2018(1998).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=BRISTOL N2;
RA Ryan E., Wohlman P., Walker C., Fielder T.;
RT "The sequence of C. elegans cosmid Y41G9A."
RL Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=BRISTOL N2;
RA Waterston R.;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AC006761; AAF60549.1;
DR InterPro; IPR001828; ANF_receptor.
DR InterPro; IPR000337; GPCR_Mgr.
DR Pfam; PF00003; 7tm_3; 1.
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DR Pfam: PF01094; ANF_receptor; 1.
DR PROSITE: PS50259; G_PROTEIN_RECEP_F3_4; 1.
SQ SEQUENCE 816 AA; 92251 MW; 4363D1LA46CBECAL CRC64;

Query Match	39.9%;	Score 1746.5;	DB 5;	Length 816;
Best Local Similarity	46.4%;	Pred. No. 3.7e-128;		

Sequence similarity	Accession no.	Length	Matches	Mismatches	Indels	Gaps
356	U00096	120	131	251	29	11

Qy	46	AGKGGWGGACMPATRLADDVNVQNPNLLPGFKLLIHSNDSCEPGLGASVWYNLLYK	105
Db	3	SGSGWAGGAEACLPAVEMALKDNRSLDILPGVYLVNNTNHSQCQQLAMQQLYDFLYP	62
Qy	106	POKMLLAGSGTCTVTAEEAAKWNLLVLCYGASSPALSDDRKEPFLFTHPSATVHNTP	165
Db	63	PTKMLMLTGCSPTVTAEEAPVWMLVVLVYSGSSPALSNNRFPFLFTHPSANNQNP	122
Qy	166	RIKLMKFGSRVAILQQAEBEVFTSTVEDLENRCMEAGVEIVTRQSFLLDPDAVNRLLR	225
Db	123	RIHIMEXFKWRFTILMSVEEVFTAKDLEATARKKGIKVDROQSFDPDAMKTLOR	181
Qy	226	QDARIIVGLFVYVVAARVLCEMYKOQLYGRAHVWFFIGTWEDWNVEVNLKABEITCTVEQ	285
Db	182	QDARIIVGLFVYVTEARVLCQAYIHGILYGRYVWFFIGTWADTWIPPEEHLNCTAEQ	240
Qy	286	MRIAAEGLHTTEALMNNONOTTISGMTABEEFHRLLNQALIEEGYDINHDRYPEGYOAP	345
Db	241	MTEAEYHTTESVNLRSRONIPALISEMTGMQOFQORUQYEFQKDTANVG-----GPPEAP	294
Qy	346	LAYDAVMSVALAFNKTMERLITGKKSURDFTYDDKEIADBIYAAAMSTOFLGVSGVVAFS	405
Db	295	LAYDAVWALAFNCTRNLLPSHIRLENFTYDNKYVIADFLFQCVKNTSPFGVSGVKMFS	353
Qy	406	SQGDRIALTOEQMIDCKEYKGLGYDQLOLNLWNLTEQWIGKKVPQDRFTIVTHVLRTV	464
Db	354	DSGDRIARTOEQMQGGKYKIMGYDITSGDLEWYNEQWLNGKGGPPDSTVYKKAHMTV	413
Qy	465	SLPLFVCMCTISSCGIFVAFALIFNIWNKHRRVIOSSHVPVCMITMLFGVILCLISVILL	524
Db	414	SNEFYPTILFVIGIAACVFYILFTQKHHERLIIFOSQPECNNILIGSCSLCLFSLFLI	473
Qy	525	GI--DGRFVSPEEYKPCIOCARAWLLSTGFTLAYGAMSKVMYVRHRE--TTKAKTDPKKV	580
Db	474	GLPDDISISLSPLLCCHARVITLLRGFTFAYGSMFAKVMIVHRMGATENQOLASROKD	533
Qy	581	EP--WKLYVMVSGLLSIDLVILLSQIFDPLQRYLETFPLEDPVSTTDDIKIRPELEHC	637
Db	534	EPISSSKFYIVAAALTADVDFVCVFWVLIDPLHLITEQKFLFPTPADSEEDIMPVLQOC	593
Qy	638	ESORNSMGLVYGFKGILLVFLGFLAYETRSIKVKOINDSRVYGMISYNNVVLCILITAP	697
Db	594	QSNQOEVMWIGLMEFKLLLVFGFTLSETNKLRIINDSRFVGLAIYNVAVMTLVITAP	653
Qy	698	-VGMVIAASQODASFAFVALAIFCCFLSMILLIFVPKVIEWIRHPKKAESKYNPD---SA	753
Db	654	VVTLLIHCKVDANFAFISLTV-----GLIYGPKRHHIIVPPPSADEQLNGNVGPV	705
Qy	754	ISKEDEERYQKLVTENEOQLRIITQKEBKIRVLQRVLVERGDAGKTE	800
Db	706	MSKVDQKRYDMLKKNETLQIIEBKERRKHECKERLEELTKNSET	752

RESULT. 4

AC	Q9BML6	PRELIMINARY;	PRT; 1220 AA.
AD	Q9BML6		
AE	Q9BML6		
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AJ	Q9BML6		
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BH	Q9BML6		
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BJ	Q9BML6		
BK	Q9BML6		
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BQ	Q9BML6		
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CO	Q9BML6		
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FJ	Q9BML6		
FK	Q9BML6		
FL	Q9BML6		
FM	Q9BML6</		

OC OC OX RN RP RX RA RT RT RL DR KW SQ

·Query Match	27.1%;	Score 1186.5;	DB 5;	Length 1220;
Best Local Similarity	32.9%;	pred. No. 5.8e-84;		
Matches 272:	Conservative 183;	Mismatches 311;	Indels 61;	Gaps 23;

QY	17	LLCLIASPHLOGVAGRPDELHIIGIIPPIA-GKGGWOGGQACMPATRLALDDVNKOPNLL	75
Db	12	LLFLLLWSTACGRATKRS-D-VYIAGFFPYDGVDSYNTGRGVMPSVKALALCHVNEHGKIL	70
QY	76	PGFKLIHNSDSECEPLGASVWYNLLYNKPKMLML-AGCSVCTVTVAAAKMWNLVL	134
Db	71	ANYRLHMMWMDTQCNAAVGVKSFDDMHSGPNKVMLFGAACHTHVTDPIAKASHHHLTQL	130
QY	135	CYGASSPALSDRKRPFTLFRTHPSATVHNPRIMKMKFGWSRVAIIQQAAEEVFI	190
Db	131	SYADTHPMFT-KDAPNFFRVVPSENAFAFNPRALLKEFNKTRVGTVQYNEPRYSLPNNH	189
QY	191	TVEDLENRCMEAGVEIVTRQSFSLDPTDVAVNLRRQDARIIVGLFVYVAARRVLCENYKQ	250
Db	190	MVADLD--AME--VEVVETQSFVNDVAESKKLREKDVRIITLGNFNEHFARKAFCEAYKL	245
QY	251	OLYGRAHVWFFIGWYEDNMYEVNLIKAEGIITCTVEQMRTAABGHLTTEALMKNQNTTIS	310
Db	246	DYIGRAYQWLLMATYSTDMWNTVQDSE--CSVBEIATALEGALTDVOLLPLSTSGDITVA	302
QY	311	GMTAEFRHRLNQALETBYD--INHDTRYPEGYQEBPLAYDAVWSVALAFNAFKTMERLT	366
Db	303	GITADEY-----LVE--YDRLRGTEYSRF-HGY-----TYDGIWAALAIQYVAEK--	345
QY	367	TKGKSLRDFTYDKEIADIYAAMNSTOFLGVSGVAFPSOGDRIALTOIQEIMDGKYEK	426
Db	346	-REDLLTHFDYRVKDWESVFEALRNTSEFGYGTVPVRFPY-NERKANILLINQOLFQOMEX	403
QY	427	LCYYDTOLD--NLSWLNTQEWIGGKVPQDRTIVTHLVTSVLPFVCMCTISSGIFPAF	484
Db	404	IGEXHSQKSHJDLDSLGKVPKWVGKTPPKDRTLLVIEHSQVNPTIIVVSASVIGVLIAT	463
QY	485	ALITIEWNKRRVTOSSHPCVNTIMLFGVTICLISVLLIDGDRFSPPEYKPCQARA	544
Db	464	VFLAENIKYRNQRYIKMSSPHLNLLIIVGCMITVLSIIFLDTTLSVAAPFYICTARA	523
QY	545	WLLSTGFTLAYGAMESKYVRVHREFTTKAOTDPKKVPEWPKLYTMVSGLLSDLVLLSWQ	604
Db	524	WILMAGESLSFGGAMESKTRVHVSIFTDLKLN-KVKYDQLFMVGVGLAIDIAIITWQ	582
QY	605	IDFPLQRYLFTPLDDPV--STTTDDIKTRPELEHCESSORNWMLGLVYGEKGLLIVGCLF	662
Db	583	IADPT--YRETQLE-PLHHEINDVLVIPENETQSEHMTIFVSIYAYKGLLVFEGAF	639
QY	663	LAYETRSIKVKOINDSRVYVGMYSIYNNVLCITAPGVGVIAQSODASFAFVALAVIFCCF	722
Db	640	LAWETRHVSIPALNDSKHIGFSYVNVFTITCLAGAAISLVSDRDKDLFVLLSFIIFCTT	699
QY	723	LSMLLIFPKVTEVIRHPKDAESKYNP-----DSAIKDEERYQKLVITNEQ	771
Db	700	ATLCLVFYPKVLELARNQGVVDKVRATLRPMKNGRRDSSVC-ELQRLRDVKNTNCR	758
QY	772	LQRLTTQKEEKIRVLQRLVERGDAGKGTELNGATGVASAAVATTSQP	818

Db 759 FRKALMEKENELOALIRKL---GPEARKWIDGVTCTGGSNVSGSELEP 802

RESULT 5

Q9Y133 PRELIMINARY; PRT; 1221 AA.

AC Q9Y133;

DT 01-NOV-1999 (TrEMBLrel. 12, Created)

DT 01-JUN-1999 (TrEMBLrel. 12, Last sequence update)

DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)

DE BCDA:GH07312 PROTEIN.

GN GABA-B-R2 OR BCDA:GH07312 OR CG6706.

OS Drosophila melanogaster (Fruit fly).

OC Eukaryota; Metazoa; Arthropoda; tracheata; Hexapoda; Insecta;

OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;

OC Ephydroidea; Drosophilidae; Drosophila.

OC NCBI_TaxID=7227;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=BERKELEY;

RA MEDLINE=20196006; PubMed=107311132;

RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,

RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,

RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,

RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,

RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,

RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,

RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,

RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,

RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,

RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,

RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,

RA Cherry J.M., Clewley S., Dahlke C., Davenport L.B., Davies P.,

RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,

RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,

RA Folsler C., Gabriellian A.C., Ferraz C., Ferreira S., Fleischmann W.,

RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,

RA Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,

RA Hostin D., Huston K.A., Howland T.J., Wei M.-H., Ibegwam C.,

RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,

RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,

RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,

RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,

RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,

RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,

RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleab J.M.,

RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,

RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,

RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,

RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,

RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,

RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissbach J.,

RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,

RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,

RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,

RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;

RT "The genome sequence of Drosophila melanogaster.";

RL Science 287:2185-2195(2000).

RN [2]

RP SEQUENCE FROM N.A.

RA Rubin G.M., Wan K.H., Harvey D., Lewis S.E., Brokstein P., Tsang G.,

RA Agbayani A., Arcina T., Baxter E., Blazej R.G., Butenhoff C.,

RA Champe M., Chavez C., Chew M., Doyle C.M., Farfan D.E., Frise E.,

RA Galle R., George R.A., Harris N.L., Hoskins R.A., Evans-Holm M.,

RA Houston K.A., Hummasti S.R., Kim E., Li P., Moshrefi M., Pacleab J.M.,

RA Park S., Sequeira A., Sethi H., Snir E., Svirskas R.R., Weinburg T.,

RA Celniker S.E.;

RT "Full length Drosophila melanogaster cDNA sequence.";

RL Submitted (APR-1999) to the EMBL/GenBank/DBJ databases.

DR EMBL; AE003736; AAF55916.1; -

DR EMBL; AF145639; AAD38614.1; -

DR FlyBase; FBgn0027575; GABA-B-R2.

DR InterPro: IPR001828; ANF_receptor.

DR InterPro: IPR000337; GPCR_Mgt.

DR Pfam: PF00003; 7tm_3; 1.

DR Pfam: PF01094; ANF_receptor; 2.

DR PROSITE: PS0259; G_PROTEIN_RECEP_F3_4; 1.

SQ SEQUENCE 1221 AA; 138123 MW; A57A9954F31FOA05 CRC64;

Query Match 27.1%; Score 1183.5; DB 5; Length 1221;

Best Local Similarity 32.8%; Pred. No. 9.9e-84;

Matches 271; Conservative 184; Mismatches 311; Indels 61; Gaps 23;

QY 17 LCLIASPHLOGGVAGRPDELHIGGIPPIA-GKGGWGGQACMPATRLALDDVAKQPNLL 75.

DB 12 LLFLLMSTACGRATKRS-D-VYIAGFFPYGDGVNSYTGRCMPSVKLALGHVNEHGKIL 70

QY 76 PGFKLILHSNDSECEPGIGASVMYLLNYPKQKMLLL-AGCSTVCTTVAEAAKWNLLVL 134

DB 71 ANYKLHMWNDDTCNAAGVGVKSFDDMHSGPNKYNLFGAACHTHVTDPIAKASKHHLTQL 130

QY 135 CYGASSPALSDRKRPFTLFRTHPSATVHNPTRIKMKKFGMSRVAILQQAAEEVFI---S 190

DB 131 SYADTHPMFT-KDAFPNFFRVVPSNAFNPRLALLKEFNTRVGYVQNEPRYSLPHNH 189

QY 191 TVEDLENRCMEAGVEIVTROSFLSDPTDAVNLRRQDARIIVGLFVYVAARRVCEMYKQ 250

DB 190 MWADLD--AME--VEVVTQSFVNDVAESLKKLREKDVRIILGNFNEHFARKAFCEAYKL 245

QY 251 QLVGRAHVWFEGIGWEDNWEVNLKAGICTVTEQMRTAAEGHLLTALMKNQNNQTTIS 310

DB 246 DMTGRAYQWIMATYSTDMWNVTODSE---CSVEIATALEGAILVDLLPLUSTSGDITVA 302

QY 311 GMTAEFRHRLNALIEEGYD---INHDRYPEGQAPLAYDAVWSVALFNKTMERLT 366

DB 303 GITADEY-----LVE--YDLRGTEYSR-HCY-----TYDGIWAALAIQYVAEK-- 345

QY 367 TGGKSLRDTYTKDAIDEIYAANNSTQFGLVGVGVAFSSQGDRIALTQIEQMDGKYEK 426

DB 346 -REDLLTHFDYRVKDWESVLEALRNTSFEQVTPVRFYN-NERKANILINQFQLGQMEK 403

QY 427 LGYDQTDLD--NLSWLATEQWIGKVPQDRTIVTHVLTSLPLFVCMCTISSCGIFVAF 484

DB 404 IGETHSQKSHLDLSLGPVKNWVGKTPPKDRTLIYIEHSQVNPTIYIVSASVIGVIAT 463

QY 485 ALIIFINWKNHRRVIOSSHPCNTIMLFGVICILSVLILGIDGRFVSPEYPRKICQARA 544

DB 464 VFLAFNLKYRNQRYIKMSSPHLNNLIIVGCMNTYLSIIFGLDITLSSVAAPFYICTARA 523

QY 545 WLLSTGFTLAYGAMFSKVRVHRFTTKAKTDPKKKVPWKLYTWVSGLLSIDLVILLSWQ 604

DB 524 WILMAGFSLSGAMFSKTRVRHSIFTDLKLN-KKVIKDYQLFMVVGVLAIADIAITWQ 582

QY 605 IFDPLQRYLTFPLEDPV--STTDDIKIRPELEHCEQSQRNSMWLGLVYGKGLLVFGLF 662

DB 583 IADPF--YRETKOLE-PLHHENIDDLVIVPENECYQSEHMTIFVSIYAYKGLLVFGAF 639

QY 663 LAYETRSIKVQLNDSRVGMSIYVNVVLCITAPVGVWIASQOQDASGAFVALAVIFCCF 722

DB 640 LANETHRVSPALNDSKHIGFSYVNVFITCLAGAAISLVLSDRKDLVFLVLSFIIFCTT 699

QY 723 LSMLLIFVPKVIIEVRHPKDKAESKYNP-----DSAIKDEDEERYQKILVTNEQ 771

DB 700 ATLCLVFVKLVKLKRNQGVQVDRKVRATLRPMKSKNGRRDSSVC-ELEQRLRDVKNTNCR 758

QY 772 LQRLITQKEKIRVLRORLVERGDAKTELNGATGCVASAAVAATTSQP 818

DB 759 FRKALMEKENELOALIRKL---GPEARKWIDGVTCTGGSNVSGSELEP 802

RESULT 6

Q9VPS7 PRELIMINARY; PRT; 1305 AA.

ID Q9VPS7

AC Q9VPS7;

DT 01-MAY-2000 (Tremblrel. 13, Created)
 DT 01-MAR-2001 (Tremblrel. 16, Last sequence update)
 DT 01-JUN-2001 (Tremblrel. 17, Last annotation update)
 DE CG3022 PROTEIN.
 GN GABA-B-R3 DR CG3022.
 DS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 OX NCBI_TaxID=7227;
 RN [1]
 RN SEQUENCE FROM N.A.
 RC STRAIN=BERKELEY;
 RX MEDLINE=20196006; PubMed=10731132;
 RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Ananides P.G., Scher S.E., Li P.W., Hoskins R.A., Galle R.F.,
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
 RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
 RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
 RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
 RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
 RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brotter P.,
 RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
 RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
 RA Folsler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
 RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
 RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 RA Laoko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang X., Lin X.,
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
 RA Shue B.C., Siden-Kimms I., Stimpson M., Skupski M.P., Smith T.,
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
 RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissbach J.,
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.D.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 RT "The genome sequence of *Drosophila melanogaster*."
 RL Science 287:2185-2195(2000).
 DR EMBL: AE003588; AAF51465.2;
 DR FlyBase; FBgn0031275; GABA-B-R3.
 DR InterPro; IPR001828; ANF_receptor.
 DR InterPro; IPR000337; GPCR_Mgr.
 DR InterPro; IPR000005; HTHarac.
 DR Pfam; PF00003; 7tm3.3; 1.
 DR Pfam; PF01094; ANF_receptor; 1.
 DR PRINTS; PR00248; GPCR_MGR.
 DR PROSITE; PS02059; G-PROTEIN_RECEPTOR_F3_4; 1.
 DR PROSITE; PS00041; HTH_ARAC_FAMILY_1; UNKNDWN_1.
 SQ SEQUENCE 1305 AA; 143588 MW; A9C3C85307650450 CRC64;

Query Match 23.4%; Score 1022.5; DB 5; Length 1305;
 Best Local Similarity 29.1%; Pred. No. 4.7e-71;
 Matches 250; Conservative 171; Mismatches 348; Indels 91; Gaps 22;

QY 41 GFFPTA-CGGGQGCACMPATRLALDDVKNQPNLLPGFKLLIHSNDSECEGLGASVMY 99
 Db 157 GLFELSTGRGPRDGLSELGAATMAVEHNRK-RLPGYTLLELVNTDQCDPGVGDVDRFF 215

QY 100 NLLYNKPKLMLL--AGCSTVCTTVAEAAKMNWNLIVLCYGASSPALSDDRKEPTFLRTH 156
 Db 216 HAIYQPTSTRMVNLGSAQSEVTEAKVVPYVIVQVSGFSTSPALSDRRFFYFRTV 275
 QY 157 PSATVINPTRIKLMKFGWSRVAILQAAEEVFISTVEDLENRCMEAGVEIVTOSF-LSD 215
 Db 276 APDSSHNPARIAIRKFGWTVITFSQNEEVHSLAVNNLVTELEAANISCAATITFAATD 335
 QY 216 PTDVAVNRLRQDARIIVGLFVYVAARVLCVMYKQQLYGRAHWFF-----IGYENWY 270
 Db 336 FKEQLLLRETDTRIIGTSFSEQLAPQILCEAYRLRMFGADYAWILHESMGAPWPD--- 392
 QY 271 EVNLKAGGITCTVEQMRIRAAEGHLLTEALMNQNNQTTISGTAEEPRHLNQAIE--- 327
 Db 393 -----QRTACSNHEQLAVENLIVVTHNSIVGNNSYSGLNNHMFNSQKQSAQPHG 446
 QY 328 -----EGY-----DINHNR-----YPEGY-QEAPLAYDAVMSVALAF 358
 Db 447 QDGFSGYSGRSIASTAQSDSRRRRGVGTSGHLFPPEAISQVAPQTYDAVVAIALAL 506
 QY 359 NKTME--RLPTGKKSLRDFYTDKEIADEIYAANNSTQFLGVSGVWAFSSQGDRIALTQI 416
 Db 507 RAAEEHWRNREEQSKLDFDYTRSDMAWEFLQMGKHLFLGVSGVPVSFSGP-DRVGTAF 565
 QY 417 EQMDGKYEKLGYDTQDNLW-----LNTQEWIGGKVPQDRTIVTHVLRVSLPLFCM 472
 Db 566 YQIRGGLLEVALYYPATDALDFRCRCPVKHSGQVPIAKRVFKLRVATIAPLAFYTI 625
 QY 473 CTISCCGIFVAFALIIENINKNHRRVIOSSHPCVNTMLFGVILCLISVILLGIDGRFV- 531
 Db 626 ATLSSVGIALAIAFLAFLNHLFRKKAIKLSPKLSNTAVGCCIFVATVILLGDHSTLP 685
 QY 532 -SPEEYKICQARAWLLSTGFTLAYGAMFSKVRVHR-FTTKAKTDPKKKVPEPKLYTMV 589
 Db 686 SAEDSPATVCTARVYLLSAGFSLAGFSNFAKTYRVHRIETRTGVSVEKDKMLQDIQLLV 745
 QY 590 SGLLSIDLVLSSQIFDPIQRYLETPLDPVSTTD-DIKIRELEHCEQSQRSMIGL 648
 Db 746 GGLLVALLVLTWVVDPMERHLNLTLE--ISATDRSVYVQVQVEVCRSQHTQTLVS 803
 QY 649 VYCFKGLILVGLFLAVETRSIKVKQINDSRVGMISYVNVVLCITAPVGMVLTASQDA 708
 Db 804 LYAFKGLLVVGVYVMAMETHRVKIPALNDSQYIGVSVTVSVTSAIVVVLNLSERVTL 863
 QY 709 SFAPVALAVIFCCFLSMLLIFVPK-----VIEIRHPKDKAESKYNPDSDAISKEDE 759
 Db 864 AFITITALITSTATLCLLFIPLKLDIWARNDIIDPVIHSMG-LKMECNTRRFVVDNR 922
 QY 760 ERYOKLVTEQELQRLTQKEEKIRVLRQLVERGDAGKTELNGATGVASAATTSQPA 819
 Db 923 ELQYRVEVQNRVYKKEIQALDAEIRKL-ERLLESG-----LTTTSTTSST 968
 QY 820 SLINSSAHATPAATLAIQOG 839
 Db 969 SLITGGGHLKP--ELTVTSG 986
 RESULT 7
 Q9BML5 PRELIMINARY; PRT; 1305 AA.
 AC Q9BML5;
 DT 01-JUN-2001 (Tremblrel. 17, Created)
 DT 01-JUN-2001 (Tremblrel. 17, Last sequence update)
 DT 01-JUN-2001 (Tremblrel. 17, Last annotation update)
 DE PUTATIVE METABOTROPIC GABA-B RECEPTOR SUBTYPE 3.
 GN GABA-B-R3.
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 OX NCBI_TaxID=7227;
 RN [1]
 RN SEQUENCE FROM N.A.

RX PubMed=11168554;
RA Mezler M., Muller T., Raming K.;
RT "Cloning and functional expression of GABA-B receptors from
RL *Drosophila*.";
RL Eur. J. Neurosci. 13:477-486(2001).
KW EMBL; AF318274; AAK13422.1; -;
SQ SEQUENCE 1305 AA; 143701 MW; 8BBA80F0E9BEADD CRC64;

Query Match 23.3%; Score 1018.5; DB 5; Length 1305;
Best Local Similarity 29.0%; Pred. No. 9,7e-71;
Matches 249; Conservative 171; Mismatches 349; Indels 91; Gaps 22;

QY 41 GIPPIA-CKGHWGQGOACMPATRIALDDVKNQPNLLPGFKLILHSNDSCEPGLGASVWY 99
Db 157 GLFELSTSRGPRDGLSELGAATMAVEHINRK-RLLPGYTLELVNTDQCPCGVGVDREFF 215
QY 100 NLLYNKPKQKMLL---AGCTVCTTVAEAAKMNLIIVLCYGASSPALSDDKRPETLFRTH 156
Db 216 HAIYTOPSTRVWMLLGSACSEVTESLAKVVPWNIVQVSFGSTSPALSDDREFFPYRTV 275
QY 157 PSATVHNPTRIKMKKFSRVAILQQAEEVFISTVEDLENRCMEAGVEIVTRQSP-LSD 215
Db 276 APDSSHNPARTAFIRKFCGCVTFYSQNEEVHSLAVNNLVTELEAANISCAATITFAATD 335
QY 216 PDAVNRRLRODARIIVGLFVYVAARRVLCEMYKOOLYGRAHWFF-----IGWYEDNMY 270
Db 336 FKEQLLLRLRETDRIIGSFQSOELAPQILCEAYRLRMFGADYAWILHESMGAPWPD--- 392
QY 271 EVNLKABGIICTVEOMRTAAEGHLLTTEALMNQNTTISGMTAEFRRLNQALIE--- 327
Db 393 -----QRTACSNHELOLAIVENLIVVSTHNSIVGNVSYSGLNHMFNSQLRKKQSAQFHG 446
QY 328 -----EGY-----DINHDR-----YPEGY-QEAPLAYDAVMSVALAF 358
Db 447 QDGFSGYGPRISTAATSDSRRRRRGVGTSGGHLFPEAISQYAPQYDVAWIALAL 506
QY 359 NKTWE--RLTTGKSLRFTYTDKEIADIYAAMNSTOFLGVGVVAFSSQGDRIALTOI 416
Db 507 RAAEEHWRNEEQKLDGDFYTRSDMAWEFLQOMKLFHFGVGVVAFSSQGDRIALTOI 565
QY 417 EQMIDGYEKLYGTYDQDLNLSW----LNTQWIGKGVPODRTIVTHVLTVSPLPFCVM 472
Db 566 YQIQGGLLEPVALYPAPDALDFRCPRCPVKHSGQVPIAKRVFKLRVATTAFLAFYTI 625
QY 473 CTISCGIFVAFALIIPIFNWKNHRRVIOSSHVPVNTIMLFGVILICLISVILLIGDGRFV- 531
Db 626 ATLSVGVIALAITFLAFNLHFRKKAIKLSSPKLSNITAVGCFIVATVILLGLDHSITLP 685
QY 532 -SPEEYPKICOARAWLLSTGFTLAYGAMFSKVMRVRH-FTTKAKTDPKKKVPEWKLTYMV 589
Db 686 SAEDSFATVCTARVYLLSAGSLAFSGMFAKTYRVHRIFTRTGVSFKDKMLQDILILV 745
QY 590 SGLLSIDLIVLLSQIFDLPQRYLETFFLPDVPSTTD-DIKIRPELHCEESQNSMWLGL 648
Db 746 GGLLVLDALLVTLVAVTDPMERHLNLTLE--ISATDRSVYVQPOVEVCRSQTQTLVSV 803
QY 649 VYGFKGLILVFLGLFAYETRSIKVKQINDSRVGVSIYVNVVLCITAPVGMVIA SQODA 708
Db 804 LYATGGLLVGVVYVWAMETRVKVLPALNDSQIGVSVYSVVITSVAVVLANLISERVTL 863
QY 709 SFAPVALAVIPCCFLSMILLIEVPK-----VTEVIRHPKDKAESKYNPDSAISKEDE 759
Db 864 AFITITALLSTATTCLLPKPLKLDIWARNDIIDPVHSMG-LKMECNTRFVVDDRR 922
QY 760 ERYOKLVTENQRLQITQKEEKIRVLQRQLVERGDAKGTGELNGATGVASAAVATTSQPA 819
Db 923 ELQYRVEQNRVYKKEIQALDAEIRKL-ERLESQ-----LTTSTTTSSST 968
QY 820 SLINSSAHATPAATLAIQOG 839
Db 969 SLITGGGHLKLP--ELTTSVG 986

RESULT 8

Q23442 ID Q23442 PRELIMINARY; PRT; 402 AA.
AC Q23442;
DT 01-NOV-1996 (Tremblrel. 01, Created)
DT 01-NOV-1996 (Tremblrel. 01, Last sequence update)
DT 01-JUN-2001 (Tremblrel. 17, Last annotation update)
DE COSMID ZK180.
GN ZK180.1.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BRISTOL N2;
RX MEDLINE=94150718; PubMed=7906398;
RA Wilson R., Ainscough R., Anderson K., Baynes C., Berks M., Coulson A.,
Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Fulton L.,
Craxton M., Dear S., Du Z., Durbin R., Favello A., Fulton L.,
Gardner A., Green P., Hawkins T., Hillier L., Jier M., Johnston L.,
Jones M., Kershaw J., Kirsten J., Laister N., Latreille P.,
Lightning J., Lloyd C., Mcmurray A., Mortimore B., O'Callaghan M.,
Parsons J., Percy C., Rifken L., Roopra A., Saunders D., Showkeen R.,
Smaldon N., Smith A., Sonhammer E., Staden R., Sulston J.,
Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K., Waterston R.,
Watson A., Weinstock L., Wilkinson-Sproat J., Wohlman P.;
RT *2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
elegans";
RL Nature 368:32-38(1994).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=BRISTOL N2;
RA Pauley A., Le T. T.;
RL Submitted (MAY-1996) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=BRISTOL N2;
RA Waterston R.;
RL Submitted (MAY-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL; U58748; AAB52965.1; -;
DR InterPro; IPR000337; GPCR_Mgr.
DR InterPro; IPR001064; Crystallin.
DR Pfam; PF00003; 7tm.3; 1.
DR PROSITE; PS00225; CRYSTALLIN_BETAGAMMA; UNKNOWN_1.
DR PROSITE; PS0259; G_PROTEIN_RECEP_F3_4; 1.
SQ SEQUENCE 402 AA; 45577 MW; D48DF0916CB4EFEE CRC64;

Query Match 10.4%; Score 457; DB 5; Length 402;
Best Local Similarity 29.9%; Pred. No. 1.7e-27;
Matches 132; Conservative 74; Mismatches 161; Indels 74; Gaps 15;

QY 389 AMNSTOFLGVGVVAFSSQGDRIALTOIEQMIDGKYEKLYGTYDQDLNLSWLN--TEQWI 446
Db 15 AIDNSFQGLTGKVKFAN-NERLGLVDIKQMSDQYVFAVDGADDEFKIIDSTTKGW- 72
QY 447 GGVPODRTIVTHVLTVSPLPFCVMCTISSCGIFVAFALIIFNWKNHRRVIOSSHVPVC 506
Db 73 --SPPLDSTITERRRHSISFLAM-----SLF-----IKMSSPNL 107
QY 507 NTMLGVIIICLSVILLGIDGRFVSPSEEPKICQARAWLLSTGFTLAYGAMFSKVMRVRH 566
Db 108 NNTIAGSICTFASVIMLGDTIRVSPDVFVWLCYTKTWTLCIGTFLSFGAMFSKTRWRH 167
QY 567 RFTTKARTOPKKVPEWKLTYMVSGLSIDLVILLSQIFDLPQRYLETFFLPDVPSTTD 626
Db 168 SIFTNTRMD-RKAIDKSKFLIIGILLFIDICVLVTFWAFVSPFS-YTVT---ELPHIPED 222
QY 627 DIKIRPELHCEESQNSMWLGLVYGFKGLILVFLGLFAYETRSIKVKQINDSRVGVMSIY 686
Db 969 SLITGGGHLKLP--ELTTSVG 986


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Db 788 SOLYNM--ILITICIVAIKTRKIP-ENFESKEIGFTWYTCIIWLAFVPIYFGTNSY 844
Qy 707 DASFAVALAVIFCCFLSMLLIFVKVIEVIRHPKDKAESKYNPDSAISKDEERYQKLV 766
Db 845 EVQTTTLCISLSASVALVCLYSPKVYTLVFP-DKNVRKLTMTNSTVYRRSAAVAQA 903
Qy 767 TENEOQLRLITQKEKIRVRLQRLVERGDAKCTE-LNG---ATGVASAAVATTSQP---- 818
Db 904 PTSSGYSRT-----HAPGTSALTGGAGVGTNASSSTLPTONSPHLDE 944
Qy 819 ASLINSSAHAT 829
Db 945 ASQTNVAHKT 955

RESULT 10
ID Q62916 PRELIMINARY; PRT; 983 AA.
AC Q62916;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE METABOTROPIC GLUTAMATE RECEPTOR 4b.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RA O'Hara P.J.;
RL Submitted (JAN-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL; U47331; AAA88788.1; -
DR InterPro; IPR000337; GPCR_Mgr.
DR Pfam; PF00003; 7tm_3; 1.
DR Pfam; PF01094; ANF_receptor; 1.
DR PRINTS; PR00248; GPCRMRG.
DR PROSITE; PS00979; G_PROTEIN_RECEP_F3_1; 1.
DR PROSITE; PS00980; G_PROTEIN_RECEP_F3_2; 1.
DR PROSITE; PS00981; G_PROTEIN_RECEP_F3_3; 1.
DR PROSITE; PS0259; G_PROTEIN_RECEP_F3_4; 1.
SQ SEQUENCE 983 AA; 109276 MW; 072F0D8B3A840A80 CRC64;

Query Match 7.9%; Score 343.5; DB 11; Length 983;
Best Local Similarity 19.08; Pred No. 5.6e-18;
Matches 170; Conservative 160; Mismatches 357; Indels 209; Gaps 35;

Qy 5 MTSQGVTFW--IFLLCLIAS-----PHLQGVVAGRP-----DELHIGGIFPIAGK 48
Db 1 MSGKGGWAWMARLPCLLLSLYAPVWPSSLGPKPGHPHNSIRIDGDTILGLFPVHGR 60
Qy 49 GWWGGQMC-----MPATRLADDVNVQNPLPGFKL----- 80
Db 61 G--SEGKACGELKKEKGTHRLEAMLFALDRINNDPOLLNITLIGARILDTCSRDTHALEQ 118
Qy 81 -----ILHSNDSECEPLGLASVMYNNLLYNKPQKLMLLAGC--STVCTTVAEAKMWNL 131
Db 119 SLTFVRLAIENKGTVEVRCGGGPP-----IITKPERVGVIGAGSGSVIMVANILRLFKI 174
Qy 132 IVLCYGASSPALSKDRKPTTLFRTHPSATVHNPTRIKLMKKGWSRVAIL-----QQA 184
Db 175 PQISYASTAPLSDNSRDFFSRVVPSTYQQAQAMVDIVRAIKWNVSTLASEGSGESG 234
Qy 185 EEVFTISTVEDLENRMEAGVEITVRSQSLSDPTDAVRNLRQDARIIVGLVYVAARRYL 244
Db 235 VEAFQKSRNGGVGVCIAQSVKIPREPKTGEEDKIIKRLLETNSARGIILFANEDDIRRVL 294
Qy 245 CEMVKKQLYGRAHWVFFIGWTEDNW-----YFVNLRKAG--ITCTVEQMRATAEGHLTT 296
Db 295 EAARRANQTGH---FFWMG--SDSWGSKSPAPVLRLEEVAEGAATILPKRMSVRGDFRYS 349
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Qy 297 EALMWNQNNOTTISGMTAEPRHRLNOALIEEGYDI-----NHDRYPE--GYOE---APLA 347
Db 350 SRTLDNRRNIWFAEFEDNEFCHKLSRHALKKGSHIKKCTNRERIGQDSAYEQBKGVQFV 409
Qy 348 YDAVWSVALAFNKMTMERLTTGKKSLRDTFTYTDKETADEIYAAMNSTQFLGYSG-VVAFSS 406
Db 410 IDAVYAMGHALHAMRDLCPGRVGL--CPRMDPVDGTQLLKYIRNVNFSGIAGNPVTENE 467
Qy 407 QGDRIALTQIEQTDGKYELGYDYDTQLDN-----LSW-----LNTQEWIGGKVP 451
Db 468 NGD-----APGRYD---IYQYQLRNGSABYKVIGSWTDLHLRIERMQWPGSGQQ 514
Qy 452 QDRTIVT-----HVLRT----- 463
Db 515 LPRSICSLPCOPGERKKTIVKGMACCHCEPCTGYQVDRYTCCTCPYDMRPTENRTSCQ 574
Qy 464 -----VSLPLFVCMCTISSGIFAFALIFNIWNKHRRVIOSSHVPNCNTIM 510
Db 575 PIPIVKLEWSDSPHVLPLFLAVVGIAAT-LEVVTFVRYN-----DTPIVKASGRELSVL 629
Qy 511 LFGVIICLSVILGIDGRFVSPPEYKPCOARAWLLSTGTFLAYGAMFSKVRVHRFTT 570
Db 630 LAGIFLCYATFLM-----IAEPD--LCTCSLRIFLGLGMSISYAAALLTKNRIYRIFE 682
Qy 571 KAK--TPPKKKVEPWKLYTWVSGLLSIDLVLILLSQWIFDPLQRYLETFPLEDPYSTTDDI 628
Db 683 QGRKRSVAPRIFSPASQALAITFILISLQLLGICVFMVVDPSHVVD---FQD--QRTLDP 737
Qy 629 KIRPELEHCESQRNSMWGLVYGFGLILVFLGLAYETRSIKVKQINDSVYVMSIYNV 688
Db 738 RFARGVLKCDI--SDLISLCLLGYSMLLMWYCTVYAIKTRGP-ETFEAKPIGFTWTT 794
Qy 689 VVLCITAPVGMVITASQDASFAFV-----ALAVIFCCFLSMLLIFVKVIEVIRH 739
Db 795 CIVWLAFIPI--FPGTSQADKLYIQITTLTVSVLSASVSLGMLYMPKVYIILFH 848

RESULT 11
Q9QYS2
ID Q9QYS2 PRELIMINARY; PRT; 879 AA.
AC Q9QYS2;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE METABOTROPIC GLUTAMATE RECEPTOR 3 PROTEIN.
GN GRM3
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=129/SV;
RX MEDLINE=20012997; Pubmed=10544282;
RA Minoshima T., Nakanishi S.;
RT "Structural organization of the mouse metabotropic glutamate receptor subtype 3 and its regulation by growth factors in cultured cortical astrocytes."
RL J. Biochem. 126:889-896(1999).
DR EMBL; AF170701; AAF06741.1; -
DR EMBL; AF170697; AAF06741.1; JOINED.
DR EMBL; AF170698; AAF06741.1; JOINED.
DR EMBL; AF170699; AAF06741.1; JOINED.
DR EMBL; AF170700; AAF06741.1; JOINED.
DR InterPro; IPR000337; GPCR_Mgr.
DR InterPro; IPR001828; ANF_receptor.
DR Pfam; PF00003; 7tm_3; 1.
DR Pfam; PF01094; ANF_receptor; 1.
DR PRINTS; PR00248; GPCRMRG.
DR PROSITE; PS00979; G_PROTEIN_RECEP_F3_1; 1.
DR PROSITE; PS00980; G_PROTEIN_RECEP_F3_2; 1.
DR PROSITE; PS00981; G_PROTEIN_RECEP_F3_3; 1.
DR PROSITE; PS0259; G_PROTEIN_RECEP_F3_4; 1.
```


Db	599	KASGRELCYILLGVFLCYCMWFI-----FIA-KPSTAVCTUURLGLGTAFSVCSYALL	655
Qy	560	SKVWRVHRFTKAKTDPKKK--VEPWKLYTMVSGLLSIDLVILLSWQIFDPLQRYLETFF	617
Db	652	TKTNRIARIFCGAREGAORPRFISPAVOAICLALISQLLIVVAMLVVEAPCTGRETAP	711
Qy	618	LEDVSTTDDDKIRPELEHESQORSNWMGLVGVFGKGLILVFLGLFAYETRSIKVKQIND	677
Db	712	ERREVWTL-----RCNHRDASMLGSLAYNV--LLIALCTLYAFKTRKCP-ENFNE	758
Qy	678	SRYGMSIYNVVVLCLITAPGVWIASOODASFAFVALAVIFCCFLSMLLIFVPKYLEVI	737
Db	759	AKFIGFTMYTTCIIWLAFLPFIYVYTSSDYRVQTTMCVSVVGLGCLFAPKLUHIL	818
Qy	738	RHPKDKAESKYNPD5	752
Db	819	FQPKNVVSHRAPTS	833
RESULT	14		
Q9PWE1	ID	Q9PWE1	PRELIMINARY; PRT; 977 AA.
AC	Q9PWE1		
DT	01-MAY-2000	(TEMBLrel. 13, Created)	
DT	01-MAY-2000	(TEMBLrel. 13, Last sequence update)	
DT	01-JUN-2001	(TEMBLrel. 17, Last annotation update)	
DE		METABOTROPIC GLUTAMATE RECEPTOR (FRAGMENT).	
GN		GLUR.	
OS		Ictalurus punctatus (Channel catfish).	
OC		Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
OC		Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi;	
OC		Siluriformes; Ictaluridae; Ictalurus.	
OX		NCBI_TaxID=7998;	
RN		[1]	
RP		SEQUENCE FROM N.A.	
RC		TISSUE=RETINA;	
RA		Helmhich H.L., Micci A.M., Sanchez X., Christensen B.N.;	
RT		"Molecular cloning, functional expression and localization of a novel	
RT		metabotropic glutamate receptor linked to calcium mobilization from	
RT		the catfish retina.";	
RL		Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.	
RL		EMBL; AF076473; AAD47893.1; -	
DR		InterPro; IPR000337; GPCR_Mgr.	
DR		InterPro; IPR001828; ANF_receptor.	
DR		Pfam; PF000003; 7tm_3; 1.	
DR		Pfam; PF01094; ANF_receptor; 1.	
DR		PRINTS; PR00248; GPCRMR.	
DR		PROSITE; PS00979; G_PROTEIN_RECP_F3_1; 1.	
DR		PROSITE; PS00981; G_PROTEIN_RECP_F3_3; 1.	
DR		PROSITE; PS50259; G_PROTEIN_RECP_F3_4; 1.	
KW		Receptor.	
FT		NON_TER.	
SEQ		SEQUENCE 977 AA; 108759 MW; BD06A67E240751CE CRC64;	
Query Match		7.5%; Score 330; DB 13; Length 977;	
Best Local Similarity		20.0%; Pred. No. 6.3e-17;	
Matches	186;	Conservative 138; Mismatches 313; Indels 292; Gaps	
Qy	14	WIFLLC-----LIASPHLQGVAGRPDELHTGGIFPIAGKGGWGGQAC-----M 58	
Db	32	WIFCVCVSPALMAHQHHPHSIKIPGDVTLGGLFPVHSGKL--GQACGEIKKKGKGVHRM 89	
Qy	59	PATRLALDDVKNQNPLLPGFL---IL-----HNSDSECEP 92	
Db	90	EAMLYALDQINSPELLPNTLTGLTRDTCSDRTYALEQSLTFVQALIQKDSIRCSNG 149	
Qy	93	LGASVMYNLLYNPKOKL--MLLAGCSTVCTVTAEAAMNWLIVLCYGASSPALSDDRKREP 150	
Db	150	-----EQPIRKPERVGVIGASASSVIMVAVNLRLFEIPOISVASTAPELSDNNRYD 203	
Qy	151	TLFRTHPSATVHNPIRKLKKFKGSRVAIL-----QQAEVFIISTVEDLENRQME 203	

Db 905 MNGGRATMTSSNGKSVSWAQNEKSSRG AHLWQRLSIHINKKE 947
|| || : | : || : : | : |

Search completed: April 30, 2002, 10:16:30
Job time: 237 sec

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OM protein - protein search, using sw model

Run on: April 30, 2002, 10:13:08 ; Search time 14.82 Seconds

(without alignments)
2078.168 Million cell updates/sec

Title: US-09-715-962-2

Perfect score: 4374

Sequence: 1 MRKDMTSDGAVTWIFLLCL.....LINSSAHATPAATLAITQGE 840

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 100059 seqs, 36664827 residues

Total number of hits satisfying chosen parameters: 100059

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_39:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	2031.5	46.4	960	1 GBR1_MOUSE	Q9wv18 mus musculus
2	2030.5	46.4	961	1 GBR1_HUMAN	Q9ubs5 homo sapien
3	2004	45.8	991	1 GBR1_RAT	Q920u4 rattus norv
4	1290	29.5	941	1 GBR2_HUMAN	Q75899 homo sapien
5	1286	29.4	940	1 GBR2_RAT	O88871 rattus norv
6	366.5	8.4	976	1 MGR_DROME	P91685 drosophila
7	361	8.3	908	1 MGR8_RAT	P70579 rattus norv
8	360	8.2	908	1 MGR8_HUMAN	O00222 homo sapien
9	356.5	8.2	912	1 MGR4_RAT	P31423 rattus norv
10	355	8.1	908	1 MGR8_MOUSE	P47743 mus musculus
11	355	8.1	915	1 MGR7_HUMAN	Q14831 homo sapien
12	353	8.1	912	1 MGR4_HUMAN	Q14833 homo sapien
13	353	8.1	915	1 MGR7_RAT	P35400 rattus norv
14	334.5	7.6	871	1 MGR6_RAT	P35349 rattus norv
15	333	7.6	879	1 MGR3_RAT	P31422 rattus norv
16	323	7.4	877	1 MGR3_HUMAN	Q14832 homo sapien
17	322	7.4	872	1 MGR2_HUMAN	Q14416 homo sapien
18	318	7.3	872	1 MGR2_RAT	P31421 rattus norv
19	313.5	7.2	877	1 MGR6_HUMAN	O15303 homo sapien
20	305	7.0	1203	1 MGR5_RAT	P31424 rattus norv
21	297.5	6.8	1212	1 MGR5_HUMAN	P41594 homo sapien
22	294	6.7	999	1 MGR1_CAEEL	O09630 caenorhabdi
23	276	6.3	1194	1 MGR1_HUMAN	Q13255 homo sapien
24	268	6.1	1199	1 MGR1_RAT	P23385 rattus norv
25	227.5	5.2	1079	1 CASR_MOUSE	Q9qy96 mus musculus
26	219.5	5.0	1078	1 CASR_HUMAN	P41180 homo sapien
27	212.5	4.9	1079	1 CASR_RAT	P48442 rattus norv
28	198.5	4.5	1085	1 CASR_BOVIN	P35384 bos taurus
29	184.5	4.2	1047	1 ANPB_RAT	P16067 rattus norv
30	181.5	4.1	1047	1 ANPB_BOVIN	P46197 bos taurus
31	177.5	4.1	1047	1 ANPB_HUMAN	P20594 homo sapien
32	172	3.9	1050	1 ANPB_ANGJA	P55202 anguilla ja
33	159	3.6	540	1 ANPC_HUMAN	P17342 homo sapien

34	156	3.6	1061	1 ANPA_HUMAN	P16066 homo sapien
35	154	3.5	535	1 ANPC_RAT	P41740 rattus norv
36	147.5	3.4	1057	1 ANPA_RAT	P18910 rattus norv
37	146	3.3	1057	1 ANPA_MOUSE	P18293 mus musculus
38	145	3.3	1137	1 CYG1_CAEEL	Q09435 caenorhabdi
39	144.5	3.3	536	1 ANPC_MOUSE	P70180 mus musculus
40	142	3.2	537	1 ANPC_BOVIN	P10730 bos taurus
41	137.5	3.1	836	1 GLK1_MOUSE	Q60934 mus musculus
42	137.5	3.1	1103	1 CYGF_BOVIN	O02740 bos taurus
43	132.5	3.0	1108	1 CYGF_HUMAN	P15841 homo sapien
44	128	2.9	918	1 GLK1_HUMAN	P39086 homo sapien
45	128	2.9	1110	1 CYGX_RAT	P51839 rattus norv

ALIGNMENTS

RESULT 1	
GBR1_MOUSE	
ID	GBR1_MOUSE STANDARD; PRT; 960 AA.
AC	Q9wv18; Q9wv15; Q9wv16; Q9wv17; Q9wv48;
DT	20-AUG-2001 (Rel. 40, Created)
DT	20-AUG-2001 (Rel. 40, Last sequence update)
DT	20-AUG-2001 (Rel. 40, Last annotation update)
DE	GAMMA-AMINOBUTYRIC ACID TYPE B RECEPTOR, SUBUNIT 1 PRECURSOR (GABA-B RECEPTOR 1) (GABA-B-R1) (GB1).
DE	GABBR1.
GN	Mus musculus (Mouse).
OS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX	NCBI_TaxID=10090;
RN	[1]
RP	SEQUENCE FROM N.A. (ISOFORM 1A).
RP	MEDLINE=20377752; PubMed=10773016;
RA	Sullivan R., Chateaufneuf A., Coulombe N., Kolakowski L.F. Jr.,
RA	Johnson M.P., Hebert T.E., Ethier N., Belley M., Metters K.,
RA	Abramovitz M., O'Neill G.P., Ng G.Y.K.;
RT	*Coexpression of full-length gamma-aminobutyric acid(B) (GABA(B))
RT	receptors with truncated receptors and metabotropic glutamate
RT	receptor 4 supports the GABA(B) heterodimer as the functional
RT	receptor.;
RT	J. Pharmacol. Exp. Ther. 293:460-467(2000).
RN	[2]
RP	SEQUENCE FROM N.A. (ISOFORMS 1B; 1C AND 1D).
RA	Younger R.;
RA	Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.
RN	[3]
RP	SEQUENCE FROM N.A. (ISOFORM 1B).
RA	Lamp K., Humeny A., Nikolic Z., Becker C.-M.;
RT	*Cloning of the murine GABABR1b receptor.;
RT	Submitted (JAN-1999) to the EMBL/GenBank/DBJ databases.
RN	[4]
RP	SEQUENCE FROM N.A. (ISOFORM 1A).
RA	Humeny A., Lamp K., Nikolic Z., Becker C.-M.;
RT	*Mouse GABA-B receptor cDNA sequence.;
RT	Submitted (JUN-1997) to the EMBL/GenBank/DBJ databases.
RN	[5]
RP	RIA-P2 INTERACTION.
RX	MEDLINE=99102694; PubMed=9872744;
RA	Kuner R., Koehr G., Gruenewald S., Eisenhardt G., Bach A.,
RA	Kornau H.-C.;
RT	*Role of heteromer formation in GABAB receptor function.;
RT	Science 283:74-77(1999).
CC	-I- FUNCTION: RECEPTOR FOR GABA. THE ACTIVITY OF THIS RECEPTOR IS
CC	MEDIATED BY G-PROTEINS THAT INHIBITS ADENYL CYCLASE ACTIVITY,
CC	STIMULATES PHOSPHOLIPASE A2, ACTIVATES POTASSIUM CHANNELS,
CC	INACTIVATES VOLTAGE-DEPENDENT CALCIUM-CHANNELS AND MODULATES
CC	INOSITOL PHOSPHOLIPIDS HYDROLYSIS. PLAYS A CRITICAL ROLE IN THE
CC	FINE-TUNING OF INHIBITORY SYNAPTIC TRANSMISSION. PRE-SYNAPTIC
CC	GABA-B-R INHIBIT NEUROTRANSMITTER RELEASE BY DOWN-REGULATING
CC	HIGH-VOLTAGE ACTIVATED CALCIUM CHANNELS, WHEREAS POSTSYNAPTIC
CC	GABA-B-R DECREASE NEURONAL EXCITABILITY BY ACTIVATING A PROMINENT
CC	INWARDLY RECTIFYING POTASSIUM (KIR) CONDUCTANCE THAT UNDERLIES THE

Qy 499 IOSHPVNCNTIMLGVIIICLVISVLLIDGRFVSPPEYKICQARAWLLSTGFTLAYGAM 558
 Db 621 IONSOPNUNNTAVGCSLALAVFLGLDGYHIGRSQFPFVCOARLWLGLGFSGLYGS 680
 Qy 559 FSKVRVHRFTTK--AKTDPKKVPKLYTMVSGLLSIDLVLLSWQIFDPQRYLETF 616
 Db 681 FTKIWWHTVFTKKEKEMKRTLEPKLYATVGLLVGMDLTLAIWQIVDPLHRTIETF 740
 Qy 617 PLEDVSTDDIKIRPELEHSCSQNSMMLGLVYGFGLILVFLGFLAYETRSIKVKQIN 676
 Db 741 AKEEKEDI-DVSIPLQLEHCSKKMTWLGIFYGVKGLLLGIFLAYETKSVSTEKIN 799
 Qy 677 DSRVYGMISYVNVVLCITAPVGMVIAOODASFVAFVALAVFCCFLSMILLIPVKVIEV 736
 Db 800 DHRAYGMAYNVAVLCITAPVTMLSSOODAFAFASIAVSSYITILVFLVFPVKMRL 859
 Qy 737 IRRHP--KDAESKYNPDISAIDEERYOKLVTEENOLQRLITOKEEKIRVLRLORLVER 793
 Db 860 ITRGEQSEADTKMTGSGSTNNNEEKSLRLEKENRELEKIITAEKERSVSELRHQLQSR 918
 RESULT 2
 GBRL_HUMAN
 ID GBRL_HUMAN STANDARD; PRT; 961 AA.
 AC Q9UBS5; Q95375; Q9U0Q0; Q96022; Q95975; Q95468;
 DT 20-AUG-2001 (Rel. 40, Created)
 DT 20-AUG-2001 (Rel. 40, Last sequence update)
 DT 20-AUG-2001 (Rel. 40, Last annotation update)
 DE GAMMA-AMINOBTYRIC ACID TYPE B RECEPTOR, SUBUNIT 1 PRECURSOR (GABA-B RECEPTOR 1) (GABA-B-R1) (GB1).
 GN GABBR1.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 [1]
 RN SEQUENCE FROM N.A. (ISOFORMS 1A AND 1B).
 RC TISSUE=Cerebellum;
 RX Kaufmann K., Schuler V., Mosbacher J., Bischoff S., Bittiger H., Held J., Froestl W., Leonhard S., Pfaff T., Karschin A., Bettler B.; "Human gamma-aminobutyric acid type B receptors are differentially expressed and regulate inwardly rectifying K+ channels."; Proc. Natl. Acad. Sci. U.S.A. 95:14991-14996(1998).
 [2]
 RN SEQUENCE FROM N.A. (ISOFORMS 1A; 1B AND 1C).
 RC TISSUE=Cerebellum;
 RX MEDLINE=99087321; PubMed=9872316;
 RA White J.H., Wise A., Main M.J., Green A., Fraser N.J., Disney G.H., Barnes A.A., Emson P., Foord S.M., Marshall F.H.; "Heterodimerization is required for the formation of a functional GABA(B) receptor."; Nature 396:679-682(1998).
 [3]
 RN SEQUENCE FROM N.A. (ISOFORM 1A).
 RC TISSUE=Brain;
 RA Stropp U., Raming K.; "Human mRNA for GABA-B1a receptor."; Submitted (OCT-1998) to the EMBL/GenBank/DBJ databases.
 [4]
 RN SEQUENCE FROM N.A. (ISOFORM 1A).
 RC TISSUE=Fetal brain;
 RX MEDLINE=98440782; PubMed=9753614;
 RA Grifa A., Totaro A., Rommens J.M., Carella M., Roetto A., Borgato L., Zelante L., Gasparini P.; "GABA (gamma-aminobutyric acid) neurotransmission: Identification and fine mapping of the human GABAB receptor gene."; Biochem. Biophys. Res. Commun. 250:240-245(1998).
 [5]
 RN SEQUENCE FROM N.A. (ISOFORM 1A).
 RX MEDLINE=99014802; PubMed=9798068;
 RA Goei V.L., Choi J., Ahn J., Bowlus C.L., Raha-Chowdhury R.,

RA Gruen J.R.; "Human gamma-aminobutyric acid B receptor gene: complementary DNA cloning, expression, chromosomal location, and genomic organization."; Biol. Psychiatry 44:659-666(1998).
 [6]
 RN SEQUENCE FROM N.A. (ISOFORM 1C).
 RC TISSUE=Cerebellum;
 RA Fraser N.J.; Submitted (OCT-1998) to the EMBL/GenBank/DBJ databases.
 [7]
 RN SEQUENCE FROM N.A. (ISOFORMS 1A AND 1B), AND VARIANTS V-20 AND S-489.
 RC TISSUE=Fetal brain;
 RX MEDLINE=20184290; PubMed=9933300;
 RA Peters H.C., Kaemmer G., Volz A., Kaupmann K., Ziegler A., Bettler B., Epplen J.T., Sander T., Riess O.; "Mapping, genomic structure, and polymorphisms of the human GABAB1 receptor gene: evaluation of its involvement in idiopathic generalized epilepsy."; Neurogenetics 2:47-54(1998).
 [8]
 RN SEQUENCE FROM N.A. (ISOFORMS 1A AND 1B).
 RA Younger R.; Submitted (JAN-1999) to the EMBL/GenBank/DBJ databases.
 [9]
 RN SEQUENCE FROM N.A. (ISOFORM 1A).
 RC TISSUE=Cerebellum;
 RX MEDLINE=99108069; PubMed=9889352;
 RA Makoff A.; "Molecular cloning of human GABAB1 and its tissue distribution."; Brain Res. Mol. Brain Res. 64:137-140(1999).
 [10]
 RN SEQUENCE FROM N.A. (ISOFORM 1E).
 RC TISSUE=Prostate;
 RX MEDLINE=20493604; PubMed=10906333;
 RA Schwarz D.A., Barry G., Eliasof S.D., Petroski R.E., Conlon P.J., Maki R.A.; "Characterization of gamma-aminobutyric acid receptor GABAB(1e), a GABAB(1) splice variant encoding a truncated receptor."; J. Biol. Chem. 275:32174-32181(2000).
 [11]
 RN VARIANTS VAL-20 AND SER-489.
 RX MEDLINE=99332183; PubMed=10402495;
 RA Sander T., Peters C., Kaemmer G., Samochowiec J., Zirra M., Mischke D., Ziegler A., Kaupmann K., Bettler B., Epplen J.T., Riess O.; "Association analysis of exonic variants of the gene encoding the GABAB receptor and idiopathic generalized epilepsy."; Am. J. Med. Genet. 88:305-310(1999).
 [12]
 RN R1A-R2 INTERACTION.
 RX MEDLINE=20237752; PubMed=10773016;
 RA Sullivan R., Chateaufneuf A., Coulombe N., Kolakowski L.F. Jr., Johnson M.P., Hebert T.E., Ethier N., Belley M., Metters K., Abramovitz M., O'Neill G.P., Ng G.Y.K.; "Coexpression of full-length gamma-aminobutyric acid(B) (GABA(B)) receptors with truncated receptors and metabotropic glutamate receptor 4 supports the GABA(B) heterodimer as the functional receptor."; J. Pharmacol. Exp. Ther. 293:460-467(2000).
 [13]
 RN R1A-R2 INTERACTION.
 RX MEDLINE=99102694; PubMed=9872744;
 RA Kuner R., Koehr G., Gruenewald S., Eisenhardt G., Bach A., Kornau H.-C.; "Role of heteromer formation in GABAB receptor function."; Science 283:74-77(1999).
 CC -1- FUNCTION: RECEPTOR FOR GABA. THE ACTIVITY OF THIS RECEPTOR IS MEDIATED BY G-PROTEINS THAT INHIBITS ADENYLYL CYCLASE ACTIVITY, STIMULATES PHOSPHOLIPASE A2, ACTIVATES POTASSIUM CHANNELS, INACTIVATES VOLTAGE-DEPENDENT CALCIUM-CHANNELS AND MODULATES INOSITOL PHOSPHOLIPASE HYDROLYSIS. PLAYS A CRITICAL ROLE IN THE FINE-TUNING OF INHIBITORY SYNAPTIC TRANSMISSION. PRE-SYNAPTIC GABA-B-R INHIBIT NEUROTRANSMITTER RELEASE BY DOWN-REGULATING

CC HIGH-VOLTAGE ACTIVATED CALCIUM CHANNELS, WHEREAS POSTSYNAPTIC
 CC GABA-B-R DECREASE NEURONAL EXCITABILITY BY ACTIVATING A PROMINENT
 CC INWARDLY RECTIFYING POTASSIUM (KIR) CONDUCTANCE THAT UNDERLIES THE
 CC LATE INHIBITORY POSTSYNAPTIC POTENTIALS. NOT ONLY IMPLICATED IN
 CC SYNAPTIC INHIBITION BUT ALSO IN HIPPOCAMPAL LONG-TERM
 CC POTENTIATION, SLOW WAVE SLEEP, MUSCLE RELAXATION AND
 CC ANTINOCICEPTION. ACTIVATED BY (-)-BACLOFEN, CGP27492 AND BLOCKED
 CC BY PHACLOFEN.
 CC
 CC -!- FUNCTION: ISOFORM 1E FUNCTION MAY BE TO REGULATE THE AVAILABILITY
 CC OF FUNCTIONAL GABA-B-RIA/GABA-B-R2 HETERODIMERS BY COMPETING FOR
 CC GABA-B-R2 DIMERIZATION. THIS COULD EXPLAIN THE OBSERVATION THAT
 CC CERTAIN SMALL MOLECULE LIGANDS EXHIBIT DIFFERENTIAL AFFINITY FOR
 CC CENTRAL VERSUS PERIPHERAL SITES.
 CC
 CC -!- COFACTOR: REQUIRES CALCIUM FOR HIGH AFFINITY BINDING TO GABA.
 CC
 CC -!- SUBUNIT: HETERODIMER OF GABA-B-R1 AND GABA-B-R2. NEITHER OF WHICH
 CC IS EFFECTIVE ON ITS OWN AND HOMODIMERIC ASSEMBLY DOES NOT SEEM TO
 CC HAPPEN. ISOFORM 1E (WITHOUT C-TERMINAL INTRACELLULAR DOMAIN) IS
 CC UNABLE TO DIMERIZE VIA A COILED-COIL INTERACTION WITH GABA-B-R2.
 CC
 CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. MOREOVER
 CC COEXPRESSION OF GABA-B-R1 AND GABA-B-R2 APPEARS TO BE A
 CC PREREQUISITE FOR MATURATION AND TRANSPORT OF GABA-B-R1 TO THE
 CC PLASMA MEMBRANE. ISOFORM 1E CAN ALSO BE SECRETED.
 CC
 CC -!- ALTERNATIVE PRODUCTS: 5 ISOFORMS: 1A (SHOWN HERE), 1B, 1C, 1D AND
 CC 1E/TRUNCATED; ARE PRODUCED BY ALTERNATIVE SPLICING. ISOFORMS
 CC CORRESPONDING TO THE FULL RECEPTOR ARE ESSENTIALLY FOUND IN THE
 CC CENTRAL NERVOUS SYSTEM (CNS). ISOFORM 1E IS THE MAJOR ISOFORM IN
 CC ALMOST ALL PERIPHERAL TISSUES. IT MAY ACT AS AN ANTAGONIST OF
 CC GABA-B RECEPTORS, BEING ABLE TO DISRUPT THE NORMAL ASSOCIATION
 CC BETWEEN ISOFORM 1A AND GABA-B-R2.
 CC
 CC -!- TISSUE SPECIFICITY: HIGHLY EXPRESSED IN BRAIN AND WEAKLY IN HEART,
 CC SMALL INTESTINE AND UTERUS. MOSTLY EXPRESSED IN GRANULAR CELL AND
 CC MOLECULAR LAYER FOR ISOFORM 1A AND IN PURKINJE CELLS FORM ISOFORM
 CC 1B. ISOFORM 1E IS PREDOMINANTLY EXPRESSED IN PERIPHERAL TISSUES AS
 CC KIDNEY, LUNG, TRACHEA, COLON, SMALL INTESTINE, STOMACH, BONE
 CC MARROW, THYMUS AND MAMMARY GLAND.
 CC
 CC -!- DOMAIN: ALPHA-HELICAL PARTS OF THE C-TERMINAL INTRACELLULAR REGION
 CC MEDIATE HETERODIMERIC INTERACTION WITH GABA-B RECEPTOR 2. THE
 CC LINKER REGION BETWEEN THE TRANSMEMBRANE DOMAIN 3 (TM 3) AND THE
 CC TRANSMEMBRANE DOMAIN 4 (TM 4) PROBABLY PLAY A ROLE IN THE
 CC SPECIFICITY FOR G-PROTEIN COUPLING.
 CC
 CC -!- SIMILARITY: BELONGS TO FAMILY 3 OF G-PROTEIN COUPLED RECEPTORS.
 CC
 CC -!- GABA-B RECEPTOR SUBFAMILY.
 CC
 CC -!- SIMILARITY: CONTAINS 2 SUSHI (SCR) DOMAINS.
 CC
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 CC -----
 CC EMBL; AJ225028; CAA12359.1; -
 CC DR EMBL; AJ225029; CAA12360.1; -
 CC DR EMBL; AJ225030; CAA12361.1; -
 CC DR EMBL; AJ225031; CAA12362.1; -
 CC DR EMBL; AJ225032; CAA12363.1; -
 CC DR EMBL; AJ225033; CAA12364.1; -
 CC DR EMBL; AJ225034; CAA12365.1; -
 CC DR EMBL; AJ225035; CAA12366.1; -
 CC DR EMBL; AJ225036; CAA12367.1; -
 CC DR EMBL; AJ225037; CAA12368.1; -
 CC DR EMBL; AJ225038; CAA12369.1; -
 CC DR EMBL; AJ225039; CAA12370.1; -
 CC DR EMBL; AJ225040; CAA12371.1; -
 CC DR EMBL; AJ225041; CAA12372.1; -
 CC DR EMBL; AJ225042; CAA12373.1; -
 CC DR EMBL; AJ225043; CAA12374.1; -
 CC DR EMBL; AJ225044; CAA12375.1; -
 CC DR EMBL; AJ225045; CAA12376.1; -
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 RP SEQUENCE FROM N.A. (ISOFORMS 1A AND 1B).
 RC STRAIN=RICO; TISSUE=Brain cortex, and Cerebellum;
 RX MEDLINE=97222131; PubMed=9069281;
 RA Kaufmann K., Hugel K., Heid J., Flor P.J., Bischoff S., Michel S.J.,
 RA McMaster G., Angst C., Bittiger H., Froestl W., Bettler B.;
 RT "Expression cloning of GABA(B) receptors uncovers similarity to
 RT metabotropic glutamate receptors.";
 RN Nature 386:239-246(1997).
 RN [2]
 RP SEQUENCE FROM N.A. (ISOFORMS 1C AND 1D).
 RC TISSUE=Cerebellum;
 RX MEDLINE=99092370; PubMed=9875211;
 RA Isumoto S., Kaibara M., Sakurai-Yamashita Y., Nagayama Y., Uezono Y.,
 RA Yano K., Taniyama K.;
 RT "Cloning and tissue distribution of novel splice variants of the rat
 RT GABA(B) receptor.";
 RN Biochem. Biophys. Res. Commun. 253:10-15(1998).
 RN [3]
 RP SEQUENCE FROM N.A. (ISOFORM 1E).
 RC STRAIN=Wistar; TISSUE=Hippocampus;
 RX MEDLINE=99388283; PubMed=10457184;
 RA Praff T., Malitschek B., Kaufmann K., Prezeau L., Pin J.-P.,
 RA Bettler B., Karschin A.;
 RT "Alternative splicing generates a novel isoform of the rat
 RT metabotropic GABA(B)R1 receptor.";
 RN Eur. J. Neurosci. 11:2874-2882(1999).
 RN [4]
 RP SEQUENCE FROM N.A. (ISOFORM 1A), AND R1A-R2 INTERACTION.
 RC TISSUE=Brain;
 RX MEDLINE=99175124; PubMed=10075644;
 RA Ng G.Y.K., Clark J., Coulombe N., Ethier N., Hebert T.E., Sullivan R.,
 RA Kargman S., Chateaufneuf A., Tsukamoto N., McDonald T., Whiting P.,
 RA Mezey E., Johnson M.P., Liu Q., Kolakowski L.F. Jr., Evans J.F.,
 RA Bonner T.I., O'Neill G.P.;
 RT "Identification of a GABAB receptor subunit, gb2, required for
 RT functional GABAB receptor activity.";
 RN J. Biol. Chem. 274:7607-7610(1999).
 RN [5]
 RP TISSUE DISTRIBUTION.
 RX MEDLINE=20121644; PubMed=10658574;
 RA Belley M., Sullivan R., Reeves A., Evans J.F., O'Neill G.P.,
 RA Ng G.Y.K.;
 RT "Synthesis of the nanomolar photoaffinity GABA(B) receptor ligand CGP
 RT 71872 reveals diversity in the tissue distribution of GABA(B) receptor
 RT forms.";
 RN Bioorg. Med. Chem. 7:2697-2704(1999).
 RN [6]
 RP R1A-R2 INTERACTION.
 RX MEDLINE=99102694; PubMed=9872744;
 RA Kuner R., Koehr G., Gruenewald S., Eisenhardt G., Bach A.,
 RA Kornau H.-C.;
 RT "Role of Heteromer Formation in GABA-B Receptor Function.";
 RN Science 283:74-77(1999).
 RN [7]
 RP MUTAGENESIS OF SER-247; SER-268 AND SER-269.
 RX MEDLINE=20159055; PubMed=10692480;
 RA Galvez T., Urwyler S., Prezeau L., Mosbacher J., Joly C.,
 RA Malitschek B., Heid J., Brabet I., Froestl W., Bettler B.,
 RA Kaufmann K., Pin J.-P.;
 RT "Ca(2+) requirement for high-affinity gamma-aminobutyric acid (GABA)
 RT binding at GABA(B) receptors: involvement of serine 269 of the
 RT GABA(B)R1 subunit.";
 RN Mol. Pharmacol. 57:419-426(2000).
 RN [8]
 RP FUNCTION: RECEPTOR FOR GABA. THE ACTIVITY OF THIS RECEPTOR IS
 CC MEDIATED BY G-PROTEINS THAT INHIBITS ADENYLYL CYCLASE ACTIVITY,
 CC STIMULATES PHOSPHOLIPASE A2, ACTIVATES POTASSIUM CHANNELS,
 CC INACTIVATES VOLTAGE-DEPENDENT CALCIUM-CHANNELS AND MODULATES
 CC INOSITOL PHOSPHOLIPIDS HYDROLYSIS. PLAYS A CRITICAL ROLE IN THE
 CC

CC FINE-TUNING OF INHIBITORY SYNAPTIC TRANSMISSION. PRE-SYNAPTIC
 CC GABA-B-R INHIBIT NEUROTRANSMITTER RELEASE BY DOWN-REGULATING
 CC HIGH-VOLTAGE ACTIVATED CALCIUM CHANNELS, WHEREAS POSTSYNAPTIC
 CC GABA-B-R DECREASE NEURONAL EXCITABILITY BY ACTIVATING A PROMINENT
 CC INWARDLY RECTIFYING POTASSIUM (KIR) CONDUCTANCE THAT UNDERLIES THE
 CC LATE INHIBITORY POSTSYNAPTIC POTENTIALS. NOT ONLY IMPLICATED IN
 CC SYNAPTIC INHIBITION BUT ALSO IN HIPPOCAMPAL LONG-TERM
 CC POTENTIATION, SLOW WAVE SLEEP, MUSCLE RELAXATION AND
 CC ANTINOCICEPTION.
 CC COFACTOR: REQUIRES CALCIUM FOR HIGH AFFINITY BINDING TO GABA.
 CC SUBUNIT: HETERODIMER OF GABA-B-R1 AND GABA-B-R2. NEITHER OF WHICH
 CC IS EFFECTIVE ON ITS OWN AND HOMODIMERIC ASSEMBLY DOES NOT SEEM TO
 CC HAPPEN.
 CC SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. MOREOVER
 CC COEXPRESSION OF GABA-B-R1 AND GABA-B-R2 APPEARS TO BE A
 CC PREREQUISITE FOR MATURATION AND TRANSPORT OF GABA-B-R1 TO THE
 CC PLASMA MEMBRANE.
 CC ALTERNATIVE PRODUCTS: 5 ISOFORMS; 1A, 1B, 1C, 1D AND 1E (SHOWN
 CC HERE); ARE PRODUCED BY ALTERNATIVE SPLICING.
 CC TISSUE SPECIFICITY: ISOFORMS 1A, 1B AND 1C ARE EXPRESSED IN
 CC TESTIS, STOMACH, SPINAL CORD AND BRAIN INCLUDING CEREBRAL CORTICAL
 CC LAYERS, PYRAMIDAL CELL LAYERS OF THE HIPPOCAMPUS, GRANULAR CELL
 CC LAYERS OF THE DENTATE GYRUS, BASAL GANGLIA, CEREBELLUM
 CC (PREDOMINANTLY IN PURKINJE CELLS FOLLOWED BY GRANULAR LAYER).
 CC ISOFORM 1B IS ALSO EXPRESSED IN KIDNEY AND LIVER. ISOFORM 1D IS
 CC EXPRESSED IN FOREBRAIN, CEREBELLUM, EYE, KIDNEY, AND URINARY
 CC BLADDER.
 CC DOMAIN: ALPHA-HELICAL PARTS OF THE C-TERMINAL INTRACELLULAR REGION
 CC MEDIATE HETERODIMERIC INTERACTION WITH GABA-B RECEPTOR 2. THE
 CC LINKER REGION BETWEEN THE TRANSMEMBRANE DOMAIN 3 (TM 3) AND THE
 CC TRANSMEMBRANE DOMAIN 4 (TM 4) PROBABLY PLAY A ROLE IN THE
 CC SPECIFICITY FOR G-PROTEIN COUPLING.
 CC SIMILARITY: BELONGS TO FAMILY 3 OF G-PROTEIN COUPLED RECEPTORS.
 CC GABA-B RECEPTOR SUBFAMILY.
 CC SIMILARITY: CONTAINS 2 SUSHI (SCR) DOMAINS.
 CC CAUTION: ISOFORM 1E HAS BEEN CALLED 1C IN REF.3.
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 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL: Y10369; CAA71398.1; -;
 CC EMBL: Y10370; CAA71399.1; -;
 CC EMBL: AB016160; BAA34708.1; -;
 CC EMBL: AB016161; BAA34709.1; -;
 CC EMBL: AF110797; AAD19656.1; -;
 CC EMBL: AF110796; AAD19656.1; JOINED.
 CC EMBL: AF110797; AAD19657.1; -;
 CC EMBL: AF110796; AAD19657.1; JOINED.
 CC EMBL: AF110797; AAD19658.1; -;
 CC EMBL: AF110796; AAD19658.1; JOINED.
 CC EMBL: AF110797; AAD19659.1; -;
 CC EMBL: AF110796; AAD19659.1; JOINED.
 CC HSSP: PI0998; 1VVC.
 CC InterPro: IPR001828; ANF_receptor.
 CC InterPro: IPR000337; GPCR_Mgr.
 CC InterPro: IPR000436; Sushi_SCR_CCP.
 CC Pfam: PF00003; 7tm_3; 1.
 CC Pfam: PF01094; ANF_receptor; 1.
 CC Pfam: PF00084; sushi; 2.
 CC PRINTS: PR01176; GABABRECEPTR.
 CC PRINTS: PR01177; GABABRECEPTR.
 CC SMART: SM00032; CCP; 2.
 CC PROSITE: PS000979; G_PROTEIN_RECEP_F3_1; FALSE_NEG.
 CC PROSITE: PS000980; G_PROTEIN_RECEP_F3_2; FALSE_NEG.
 CC PROSITE: PS000981; G_PROTEIN_RECEP_F3_3; FALSE_NEG.
 CC PROSITE: PS00259; G_PROTEIN_RECEP_F3_4; 1.
 CC G-protein coupled receptor; Transmembrane; Glycoprotein; Signal;
 CC Postsynaptic membrane; Coiled coil; Repeat; Alternative splicing.
 KW


```
Query Match          29.5%; Score 1290; DB 1; Length 941;
Best Local Similarity 33.9%; Pred. No. 6.2e-91;
Matches 286; Conservative 170; Mismatches 332; Indels 56; Gaps 18;

QY 18 LCLIASPHLQGVAGRP-----DELHIGGIFPI---ACKGSGWOGQACMPATRLALDDV 68
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 31 LLLPLAPGAWGARGAPPPSPSPLSIMGLPLTKEVAKGSI--GRGVLPVAVELAIEQI 88
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 69 NKQPNLLPGFKLLHNSDSEPGGLGASVYNNLLYNKPKLMLLAG-CSTVCTTVAEAAK 127
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 89 RNESLLRPF-IDLRLYTECDNAGLKAFYDAIKYGNPMLMVFGVCSVSIIESLQ 147
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 128 MNVLVLCYGASSPALSDDKREPTFLTRHPSATVHNPTRIKLMKKFGWRSVAILQOAEV 187
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 148 GWNVLQSFSAATTPVLADKKKYPYFERTVPSDNAVNPAILKLLKHQWKRVGTLTODVQ 207
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 188 FISTVEDLENRCMEAGVELVTRQSFSLDPTDAVNRRLRODARIIVGLFYVVAARRVLC 247
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 208 FSEVRNLTGLVGEDIEISDESFSNDPCTSVKLLKGNDRVRIILQGFQDNMAAKVFCCA 267
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 248 YKOOLYGRAHVWFFTCGWYEDNVE-VNLKAEGITCTVEOMRTAAEGHLTTEALMWNQ 306
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 268 YEENYIGSKYQIILPGWYEPWVEQVHTTEANSRCLRNKLLAAMEGYIGVDFEPLSKQI 327
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 307 TTISGMTAEFRHRLNQALIEEGYDINHDPYEGYQEAFLAYDAVMSVALAFNKTWERL- 365
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 328 KTISCKTPOOYEREYNNKSGVGPSEK- ----GY-----AYDGIWVIKTLQRMETLH 377
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 366 -TTGKKSURDYTTKEIADEIYAAMNSTOFLGVSGVAFSPGQDRIALTOIEQIDGKY 424
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 378 ASSRHQIQDFNYDHTLGRILLNAMNETNFFGVTVGVVFRN-GERMGTKFTQFODSRE 436
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 425 EKLGYDQDLNLSLN-TEQWIGKGVPODRITVTHVLTVSLPFCVCMCTISSCGIFVA 483
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 437 VKVGEINAVADTLEINDTIRFOGSEPPDKTILDLQRLKRIISLPLYSILSALTILG 496
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 484 FALIIFNIWKNHRRVQSSHPVCNTIMLFGVILICLSVILLGIDGRFVSPPEEYPKICQ 543
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 497 SAFLFENIKNRNOKLIKMSPPYNNLLIILGMLSYASIFLFGDGSFVSEKTFETLCTVR 556
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 544 AWLLSTGFTLAYGAFSKVWRVHRFTTKAKDPKKVPEWPKLVYVSGLLSIDLVILLWS 603
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 557 TWILVGVYTAFAAMFAKTRWRHAIFKPKVKM-KKKLIKQDKLVIVGGMLLIDLCILICW 615
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 604 QIFDPLQRYLETPELE-DPVSTTDLIKIRPELEHCEFSQNSMWLGLVYGFGLILVGLF 662
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 616 QAVDPLRRTVEXYSEPDPAGR--DISIRPLEHCENTHMTIWGLVYATKGLMLFPGCF 673
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 663 LAYETRSIKVKOINDSRVYGMSTYNNVVLCLITAPVGMVIAOQDASFAFVALAVIFCCF 722
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 674 LAWETRNVSIPALNDSKYIGMSVYNGVINGICAAVSFLTRDQPNVQFCIVALVIFCST 733
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 723 LSNLLIFVPKVEIVRHP-----KDKAESKNPD-SAIKSEDEERYOKLV 767
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 734 IFLCVFVFKLITRNPDAATQNRFRFQTNQKEDSKTSTSVTSVNOASTSRLEGLQS 793
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 768 ENQOLRLITQKEEKLRLVRLVERGDAKT-----ELNGATCVASAAVATTSQPA 819
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 794 ENHRUMKITELDKDLEEVMTQMDTPE-KTYYIKONHYOELNDILNLTFTSTGGKA 852
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 820 SLIN 823
   | |
Db 853 ILKN 856

RESULT 5
GBR2_RAT
ID GBR2_RAT STANDARD; PRT; 940 AA.
AC O88871: Q9QWU2; Q9JK36;
DT 20-AUG-2001 (Rel. 40, Created)
DT 20-AUG-2001 (Rel. 40, Last sequence update)
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DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE GAMMA-AMINOBUTYRIC ACID TYPE B RECEPTOR, SUBUNIT 2 PRECURSOR (GABA-B
DE RECEPTOR 2) (GABA-B-R2) (GB2) (GABABR2).
GN GABBR2.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Hypothalamus;
RX MEDLINE=99087320; PubMed=9872315;
RA Jones K.A., Borowsky B., Tamm J.A., Craig D.A., Durkin M.M., Dai M.,
RA Yao W.-J., Johnson M., Gunwaldsen C.A., Huang L.-Y., Tang C., Shen Q.,
RA Salton J.A., Morse K., Laz T., Smith K.E., Nagarathnam D., Noble S.A.,
RA Branchek T.A., Gerald C.;
RT "GABA(B) receptors function as a heteromeric assembly of the subunits
RT GABA(B)R1 and GABA(B)R2";
RL Nature 396:674-679(1998).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain cortex, and Cerebellum;
RX MEDLINE=99087322; PubMed=9872317;
RA Kaupmann K., Malitschek B., Schuler V., Heid J., Froestl W., Beck P.,
RA Mosbacher J., Bischoff S., Kulik A., Shigemoto R., Karschin A.,
RA Bettler B.;
RT "GABA-B receptor subtypes assemble into functional heteromeric
RT complexes";
RL Nature 396:683-687(1998).
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain cortex;
RX MEDLINE=20193514; PubMed=10727622;
RA Clark J.A., Mezey E., Lam A.S., Bonner T.I.;
RT "Distribution of the GABA(B) receptor subunit gb2 in rat CNS.";
RL Brain Res. 860:41-52(2000).
RN [4]
RP SEQUENCE FROM N.A.
RC TISSUE=Hypothalamus;
RX Borowsky B., Laz T., Gerald C.;
RL Submitted (JAN-1999) to the EMBL/GenBank/DBDJ databases.
RN [5]
RP RIA-R2 INTERACTION, AND VARIANTS TYR-337 AND PRO-19 INS.
RC TISSUE=Hippocampus;
RX MEDLINE=99102694; PubMed=9872744;
RA Kuner R., Koehr G., Gruenewald S., Eisenhardt G., Bach A.,
RA Kornau H.-C.;
RT "Role of Heteromer Formation in GABA-B Receptor Function.";
RL Science 283:74-77(1999).
CC -1- FUNCTION: RECEPTOR FOR GABA. THE ACTIVITY OF THIS RECEPTOR IS
CC MEDIATED BY G-PROTEINS THAT INHIBITS ADENYL CYCLASE ACTIVITY,
CC STIMULATES PHOSPHOLIPASE A2, ACTIVATES POTASSIUM CHANNELS,
CC INACTIVATES VOLTAGE-DEPENDENT CALCIUM CHANNELS AND MODULATES
CC INOSITOL PHOSPHOLIPIDS HYDROLYSIS. PLAYS A CRITICAL ROLE IN THE
CC FINE-TUNING OF INHIBITORY SYNAPTIC TRANSMISSION. PRE-SYNAPTIC
CC GABA-B-R INHIBIT NEUROTRANSMITTER RELEASE BY DOWN-REGULATING
CC HIGH-VOLTAGE ACTIVATED CALCIUM CHANNELS, WHEREAS POSTSYNAPTIC
CC GABA-B-R DECREASE NEURONAL EXCITABILITY BY ACTIVATING A PROMINENT
CC INWARDLY RECTIFYING POTASSIUM (KIR) CONDUCTANCE THAT UNDERLIES THE
CC LATE INHIBITORY POSTSYNAPTIC POTENTIALS. NOT ONLY IMPLICATED IN
CC SYNAPTIC INHIBITION BUT ALSO IN HIPPOCAMPAL LONG-TERM
CC POTENTIATION, SLOW WAVE SLEEP, MUSCLE RELAXATION AND
CC ANTINOCICEPTION.
CC -1- SUBUNIT: HETERODIMER OF GABA-B-R1 AND GABA-B-R2. NEITHER OF WHICH
CC IS EFFECTIVE ON ITS OWN AND HOMODIMERIC ASSEMBLY DOES NOT SEEM TO
CC HAPPEN.
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. MOREOVER
CC COEXPRESSION OF GABA-B-R1 AND GABA-B-R2 APPEARS TO BE A
CC PREREQUISITE FOR MATURATION AND TRANSPORT OF GABA-B-R1 TO THE
CC PLASMA MEMBRANE.
CC -1- TISSUE SPECIFICITY: EXPRESSED IN BRAIN CORTEX, HIPPOCAMPUS, MEDIAL
CC HABENULA, THALAMUS AND CEREBELLUM. COEXPRESSION IS SEEN IN
CC CEREBELLUM.
```


GN GRM8 OR GPRC1H OR MGLURB.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97168760; PubMed=9016353;
RA Saugstad J.A., Kinzie J.M., Shinohara M.M., Segerson T.P.,
RA Westbrook G.L.;
RT "Cloning and expression of rat metabotropic glutamate receptor 8
RT reveals a distinct pharmacological profile.";
RL Mol. Pharmacol. 51:119-125(1997).
CC - FUNCTION: RECEPTOR FOR GLUTAMATE. THE ACTIVITY OF THIS RECEPTOR
CC IS MEDIATED BY A G-PROTEIN THAT INHIBITS ADENYLATE CYCLASE
CC ACTIVITY.
CC - SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC - TISSUE SPECIFICITY: PROMINENT EXPRESSION IN OLFACTORY BULB,
CC PONTINE GRAY, LATERAL RETICULAR NUCLEUS OF THE THALAMUS, AND
CC PERIFORM CORTEX. LESS ABUNDANT EXPRESSION IN CEREBRAL CORTEX,
CC HIPPOCAMPUS, CEREBELLUM, AND MAMMILLARY BODY.
CC - SIMILARITY: BELONGS TO FAMILY 3 OF G-PROTEIN COUPLED RECEPTORS.
CC
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL: U63288; AB09537.1; -
CC GCRdb; GCR_1411; -
CC InterPro; IPR001828; ANF_receptor.
CC InterPro; IPR000337; GPCR_Mgr.
CC Pfam; PF000003; 7tm.3; 1.
CC Pfam; PF01094; ANF_receptor; 1.
CC PRINTS; PR00248; GPCR_MGR.
CC PRINTS; PR00593; MTABOTROPICR.
CC PRINTS; PR01058; MTABOTROPICR.
CC PROSITE; PS00979; G_PROTEIN_RECF_3_1; 1.
CC PROSITE; PS00980; G_PROTEIN_RECF_3_2; 1.
CC PROSITE; PS00981; G_PROTEIN_RECF_3_3; 1.
CC PROSITE; PS00982; G_PROTEIN_RECF_3_4; 1.
CC PROSITE; PS02059; G_PROTEIN_RECF_3_4; 1.
CC G-protein coupled receptor; Transmembrane; Glycoprotein; Signal;
CC Multigene family; Olfaction.
CC SIGNAL 1 33 POTENTIAL.
CC CHAIN 34 908 METABOTROPIC GLUTAMATE RECEPTOR 8.
CC DOMAIN 34 583 EXTRACELLULAR (POTENTIAL).
CC TRANSMEM 584 608 I (POTENTIAL).
CC DOMAIN 609 620 CYTOPLASMIC (POTENTIAL).
CC TRANSMEM 621 641 II (POTENTIAL).
CC DOMAIN 642 647 EXTRACELLULAR (POTENTIAL).
CC TRANSMEM 648 658 III (POTENTIAL).
CC DOMAIN 659 695 CYTOPLASMIC (POTENTIAL).
CC TRANSMEM 696 716 IV (POTENTIAL).
CC DOMAIN 717 746 EXTRACELLULAR (POTENTIAL).
CC TRANSMEM 747 768 V (POTENTIAL).
CC DOMAIN 769 781 CYTOPLASMIC (POTENTIAL).
CC TRANSMEM 782 803 VI (POTENTIAL).
CC DOMAIN 804 818 EXTRACELLULAR (POTENTIAL).
CC TRANSMEM 819 843 VII (POTENTIAL).
CC DOMAIN 844 908 CYTOPLASMIC (POTENTIAL).
CC CARBOHYD 95 95 N-LINKED (GLCNAC. .) (POTENTIAL).
CC CARBOHYD 298 298 N-LINKED (GLCNAC. .) (POTENTIAL).
CC CARBOHYD 452 452 N-LINKED (GLCNAC. .) (POTENTIAL).
CC CARBOHYD 480 480 N-LINKED (GLCNAC. .) (POTENTIAL).
CC CARBOHYD 565 565 N-LINKED (GLCNAC. .) (POTENTIAL).
CC SEQUENCE 908 AA; 101866 MW; FCAB54CB8E3DD915 CRC64;

Query Match 8.3%; Score 361; DB 1; Length 908;
Best Local Similarity 21.0%; Pred. No. 1.3e-19;

Matches 204; Conservative 154; Mismatches 374; Indels 238; Gaps 45;
QY 13 FWIFLCLLIASHPHLQGGVAG-RPD-ELHTGGTFPIAGKGGWGOAC-----MP 59
DB 22 YWI--LTMQTHSQEYAHSRVGDGDIILGGLFPVHAKG--ERGVPCKELKEKGHIHLE 77
QY 60 ATRLALDDVNRKQNPILLPGFKL--IL-----HSNDSCEPGL 93
DB 78 AMLVAIQINKDPDLLSNITLGVRLDTCSDTYALEQSLTFVQALIEKSDVRCANGD 137
QY 94 GASVYNLLYWKPKL--MLLAGCSTVCTTVAEAAKMMNLIVLCYGASSPALSDRRRPT 151
DB 138 PP-----IFTKPKDISGVIAGAAASSVMANILRLFKIPQISVASTAPELSDNTRFV 191
QY 152 LFRTHPSATVHNPRIKLMKFKGHSRVALLOQAEVFFISTVEDLENRCME-AGVEIVTRQ 210
DB 192 FSRVPPDSYQAQAMVDIVTALGMNVYSTLASEGNYGSEGVAEFTQISREIGGVIAQSQ 251
QY 211 SFLSDPTDA-----VRLRRQDARIIVGLFVVAARRVLCMEYKQQLYGRAHVWFFIGW 264
DB 252 KIPREPRGFEKIKRLETPNARAVINFANEDDIRILEAAKKNQSGH---FLWIG- 307
QY 265 YEDNW-----YEYNLKAEGITCTVEQMRTAAEG---HLTTEALMWNQNNOTTISGMTA 314
DB 308 -SDSWGSKIAPVYQEEETAEAG-AVTILPKRASIDGDFRYSRTLANRRNV---WFA 360
QY 315 EEPHRLNQALIEGYDINHRYPEGY-----QEAPLAY--DAVMSVALAFNMTM 362
DB 361 EFWEENEFGCKLGGHGRNSHIKCTGLERIAARDSSEYQEGKVQFVIDAVYSMAYLHNH 420
QY 363 ERLTYGKSL--RDTYTDKEIADEIYAAMNSTQPLGVSGV-VAFSSQGDRIALTQIBQ- 418
DB 421 KERPQYIGLCPRMVTIDGKELLYIRA-----VNFNGSAGTPTVTNENGADAPRYDIFY 476
QY 419 MIDCK--YEKLYGYDTOL-----DNLSWLNTQEWIGGKVPQDRTIVTVLRLVSLP- 467
DB 477 QINNKSTEYKIIGHWTNQLHLKVEDMQWANEH-----THPASVCSLPCPKPG 523
QY 468 -----LFVCMCTI-----SSC----- 478
DB 524 ERKKTGVGPCWHCEGCEGYNQVDELSCELCPLDQRPINRTGCQRIPIIKLEHSPW 583
QY 479 ---GIFVA-----FALIIFNIWNKHRRVIOSSHPCVNTIMLFGVILCLISVILLGID 527
DB 584 AVVPVFIALLGIIATTFVITFVRYN-DTPIVRASGRELSYVLLTGIFLCYSITFLM--- 639
QY 528 GRFVSPEEYPKICOARAWLLSTGFTLAYGAMESKVMVRHRTTKAK---TDPKKKVEPWK 584
DB 640 --IAAPDTI--ICSFRTIFGLGMCFSYAALLTKNRIHRIFEQKKSVTAP-KEISPAS 694
QY 585 LYTMSVGLSLDLVILLSQWIFDP---LQRYLETPLPDDVPVSTTDDIKIRPELEHESQR 641
DB 695 QLVITFSLISVQLLGVPVFWVVDPPHTIIDYGEQRTL-DPENARGVLK-----CDISD 746
QY 642 NSMWLGLVYGPGLILVFGLEFLAYETRSIKVKQINDSRVMSIYNNVVLCILITAPGVW 701
DB 747 LSLICSL--GYSILLMVTCTVYAIKTRGPV-ETFEAKPIGFTMTTTCIIWLAFIPFG 803
QY 702 LASOODASF---AFVALAVIFCCFLSMILLIFVPKVIEWIRHPKDKAESKYNPDSAISKED 758
DB 804 TAQSAEKMYIQTTLTVTMSLSLSASVSGLMGLYKPKYIIIFHPQNVQNR----- 852
QY 759 EERYQKLVTEQEQRLITQKEEKIRVLRQLRVERGDAKTELGATGVASAAVATTSPQ 818
DB 853 KRSEKAVVTAATMSKLIQKGNDR-----PNGEVK-SEL-----CESLETWTSSTK 897
QY 819 ASLINSASHA 828
DB 898 TTYISYNSHS 907

RESULT 8
MGR8_HUMAN

ID MGR8_HUMAN STANDARD; PRT; 908 AA.
AC 000222; O15493; 095945; 095946;
DT 01-NOV-1997 (Rel. 35, Created)
DT 20-AUG-2001 (Rel. 40, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE METABOTROPIC GLUTAMATE RECEPTOR 8 PRECURSOR.
GN GRM8 OR GPCR1H OR MGLUR8.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM A).
RX MEDLINE=98141892; PubMed=9473604;
RA Wu S., Wright R.A., Rockey P.K., Burgett S.G., Arnold J.S.,
RA Rostek P.R. Jr., Johnson B.G., Schoepf D.D., Belagaje R.M.;
RT "Group III human metabotropic glutamate receptors 4, 7 and 8:
RT molecular cloning, functional expression, and comparison of
RT pharmacological properties in RGT cells.";
RL Brain Res. Mol. Brain Res. 53:88-97(1998).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORM A).
RX MEDLINE=97446143; PubMed=9299241;
RA Scherer S.W., Soder S., Duvoisin R.M., Huizenga J.J., Tsui L.-C.;
RT "The human metabotropic glutamate receptor 8 (GRM8) gene: a
RT disproportionately large gene located at 7q31.3-q32.1.";
RL Genomics 44:232-236(1997).
RN [3]
RP SEQUENCE FROM N.A. (ISOFORMS B AND C).
RC TISSUE=Fetal brain;
RA Malherbe P., Kratzelisen C., Lundstrom K., Richards J.G., Faull R.L.M.,
RA Muter V.;
RT "Cloning and functional expression of alternative spliced variants of
RT the human metabotropic glutamate receptor 8.";
RL Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: RECEPTOR FOR GLUTAMATE. THE ACTIVITY OF THIS RECEPTOR
CC IS MEDIATED BY A G-PROTEIN THAT INHIBITS ADENYLATE CYCLASE
CC ACTIVITY.
CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC -!- ALTERNATIVE PRODUCTS: 3 ISOFORMS: A (SHOWN HERE), B AND C; ARE
CC PRODUCED BY ALTERNATIVE SPLICING.
CC -!- SIMILARITY: BELONGS TO FAMILY 3 OF G-PROTEIN COUPLED RECEPTORS.
CC
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CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -
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CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC
CC EMBL: U92459; AAB51764.1; -
CC EMBL: U95025; AAB72040.1; -
CC EMBL: AJ236921; CAB36968.1; -
CC EMBL: AJ236922; CAB36969.1; -
CC GCRdb: GCR_1889; -
CC GCRdb: GCR_2604; -
CC MIM: 601116; -
CC InterPro: IPR001828; ANF_receptor.
CC InterPro: IPR000337; GPCR_Mgr.
CC Pfam: PF00003; 7tm_3; 1.
CC Pfam: PF01094; ANF_receptor; 1.
CC PRINTS: PR00248; GPCRMR.
CC PRINTS: PR00593; MTABOTROPICR.
CC PRINTS: PR01058; MTABOTROPICR.
CC PROSITE: PS00979; G_PROTEIN_RECEP_F3_1; 1.
CC PROSITE: PS00980; G_PROTEIN_RECEP_F3_2; 1.
CC PROSITE: PS00981; G_PROTEIN_RECEP_F3_3; 1.
CC PROSITE: PS00981; G_PROTEIN_RECEP_F3_4; 1.
CC PROSITE: PS00981; G_PROTEIN_RECEP_F3_5; 1.
CC G-protein coupled receptor; Transmembrane; Glycoprotein; Signal;
KW Multigene family; Olfaction; Alternative splicing.
FT SIGNAL 1 33
FT CHAIN 34 908 METABOTROPIC GLUTAMATE RECEPTOR 8.

DOMAIN 34 583
TRANSSEM 584 608
DOMAIN 609 620
TRANSSEM 621 641
DOMAIN 642 647
TRANSSEM 648 668
DOMAIN 669 695
TRANSSEM 716 716
DOMAIN 717 746
TRANSSEM 747 768
DOMAIN 769 781
TRANSSEM 782 803
DOMAIN 804 818
TRANSSEM 819 843
DOMAIN 844 908
CARBOHYD 95 95
CARBOHYD 298 298
CARBOHYD 452 452
CARBOHYD 480 480
CARBOHYD 565 565
VARSPPLIC 893 908
VARSPPLIC 454 501
VARSPPLIC 502 908
CONFLICT 194 194
CONFLICT 460 460
CONFLICT 642 642
CONFLICT 768 768
CONFLICT 904 904
SQ SEQUENCE 908 AA; 101740 MW; 95C2D5883DAF6FDE CRC64;
Query Match 8.2%; Score 360; DB 1; Length 908;
Best Local Similarity 21.1%; Pred. No. 1.5e-19;
Matches 204; Conservative 153; Mismatches 378; Indels 232; Gaps 44;
Qy 13 FWIFLLCIASPHLOGGVAG-RPD-ELHIGGIFFIAGKGGWGGQAC-----MP 59
Db 22 YVI--LTMWORTHSEYAHSTRVDGDIILGLFPVHAK--ERGVPCGELKKEKGHRL 77
Qy 60 ATRALADVDVKNPILPGFKL---IL-----HSNDSECEPGL 93
Db 78 AMLYAIDQINKDPDLLNLTGLVRILDTCSRDYALEQSLTFVQALIEKXDSKVCANGD 137
Qy 94 GASVMYLLNYPKQL--MLLAGCSTVCTTVAEAKMWNILVLCYGASSPALSDDRFP 151
Db 138 PP-----IFTKPKDISGIVGAASVSIMVANILRLFKIPQISYASTAPELSDNTRYDF 191
Qy 152 LFRTHPSATVHNPTRIKLMKFGWSRVATLQQAEEVFISTVEDLENRCME-AGVEIVTRQ 210
Db 192 FSRVPPDSYQAQAMVDIVTALGNVYVTLASEGNYGESGVEAFTQISREIGVCIAQSO 251
Qy 211 SFLSDPTDA-----VRNLRDODARIIVGLFYVVAARRVLCEMYKQOLYGRAHVWPF 264
Db 252 KIPREPRCEFEKIKRLLETPNARAVINFANEDDIRILEAAKLNQSH---FLWIG- 307
Qy 265 YEDNW-----YEVNKAEGTCTVEOMRIAAEG---HLTTEALMMNNQNTTISGM 314
Db 308 -SDSWGSKIAPVYQEEIAEG-AVTILPKRASIDGDFRFRSRTLANRRNV-----WFA 360
Qy 315 EEFRLRLQAIEEGYDINHDPYEGY-----QEAPLAY--DAVSVAFANFKTM 362
Db 361 EFWEENFGCKLGGHGRKNSHIKKTGLERARDSSYEQEGKVQFVDAYVSMAYALHNMH 420
Qy 363 ERLTYGKKSL--RDFTYTDKEIADEIYAAMNSTOFLGVSGV-VAFSSOGDRIALTOIEO- 418
Db 421 KDLCPGYIGLCPRMSTIDGKELLYIRA-----VFNMGSAETPTVFNMGADPGRDYDF 476
Qy 419 MIDGK---YEKLGYYDTQL-----DNLSWLTNTEQWIGGKVPQDRTIYTHVLTVSLP- 467
Db 477 QITNKSTYKVGHWNTNOLHLKVEDQWVHREH-----THPASVCSLPCPKPG 523

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QY 468 -----LFCVCMCTI-----SSC----- 478
Db 524 ERKTKVGPCCWCHCERCEGYNQVDELSCELCPLDQRPNNMRTGCOLPIIKLEHSPW 593
QY 479 ---GIFVA-----FALLIFNIWNKRRRVIOSSHVPVCNTIMLFGVVIICLISVILLGID 527
Db 584 AVVPVEVAILGIIATTFVIVFVRYN-DTPIVIRASGRELSYVLLTGIFLCYSITFLM--- 639
QY 528 GRFVSPPEYPIKQARAWLLSTGFTLAGMPSKVMVRHRTTKAK---TDPKKKVEPWK 584
Db 640 --IAADPTI--ICSPRRVFLGLGCMCFSAALLTKTNRHRIHFEQGRKSVTAP-KFTSPAS 694
QY 585 LYTWSGILLSIDLVLSSQIFDPLORILEPTPELDPVSTDDIKIRPELEHCESSORNSM 644
Db 695 QLVITFSLISVOLLGVFVFWVDDPHIID----YGEORTLDPKARGVLK-CDISDLSL 749
QY 645 WLGLVYFGKILVFLGLAVETRSIKVQINDSRVYVGSINVVVLCILITAPVGMVIAS 704
Db 750 ICSL-GYSILLMVTCTVYAKTRGVP-ETFEAKPIGFTMYTTCIIWLAFIPFEGTAQ 806
QY 705 QODASF---AFVALAVIFCCFLSMILLIFVPKVIEWIRHPKDKAESKYNPDSSAISKEDEER 761
Db 807 SAEKMYIQTTTLTSSMSLSASVSLGMLYMPKVYIIIFHPQNVQKR-----KRS 855
QY 762 YOKLVTEHQRLQITQKEEKIRVLRQRLVERGDGAKGTGLNGATGVASAAVATTSOPASL 821
Db 856 FKAVVTAATMOSKLIQKGNDR-----PNGEVK-SEL-----CESLETNTSSTKTTY 900
QY 822 INSSAHA 828
Db 901 IYSNHS 907

RESULT 9
MGR4_RAT
ID MGR4_RAT STANDARD; PRT; 912 AA.
AC P31423;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE METABOTROPIC GLUTAMATE RECEPTOR 4 PRECURSOR.
GN GRM4 OR GPRC1D OR MGLUR4.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=92110002; PubMed=1309649;
RA Tanabe Y., Masu M., Ishii T., Shigemoto R., Nakanishi S.;
RT "A family of metabotropic glutamate receptors.";
RL Neuron 8:169-179(1992).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=93332699; PubMed=8338667;
RA O'Hara P.J., Sheppard P.O., Thøgersen H., Venezia D., Haldeman B.A.,
RA McGrane V., Houamed K.M., Thomsen C., Gilbert T.L., Mulvihill E.R.;
RT "The ligand-binding domain in metabotropic glutamate receptors is
RT related to bacterial periplasmic binding proteins.";
RL Neuron 11:41-52(1993).
CC -1- FUNCTION: RECEPTOR FOR GLUTAMATE. THE ACTIVITY OF THIS RECEPTOR
CC IS MEDIATED BY A G-PROTEIN THAT INHIBITS ADENYLATE CYCLASE
CC ACTIVITY.
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC -1- TISSUE SPECIFICITY: IS WIDELY DISTRIBUTED IN THE CNS. PREDOMINANT
CC EXPRESSION IS SEEN IN THE GRANULE CELLS OF THE CEREBELLUM.
CC -1- SIMILARITY: BELONGS TO FAMILY 3 OF G-PROTEIN COUPLED RECEPTORS.
CC STRONGEST, TO MGLUR6.
CC
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; M92077; NOT_ANNOTATED_CDS.
DR EMBL; M90518; AAA93190.1; -.
DR PIR; JH0563; JH0563.
DR GCRDB; GCR_0352; -.
DR GCRDB; GCR_0363; -.
DR InterPro; IPR001828; ANF_receptor.
DR InterPro; IPR000337; GPCR_Mgr.
DR Pfam; PF00003; 7tm_3; 1.
DR Pfam; PF01094; ANF_receptor; 1.
DR PRINTS; PR00248; GPCRMR.
DR PRINTS; PR00593; MTABOTROPICR.
DR PRINTS; PR01054; MTABOTROPICR.
DR PROSITE; PS00979; G_PROTEIN_RECEP_F3_1; 1.
DR PROSITE; PS00980; G_PROTEIN_RECEP_F3_2; 1.
DR PROSITE; PS00981; G_PROTEIN_RECEP_F3_3; 1.
DR PROSITE; PS0259; G_PROTEIN_RECEP_F3_4; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein; Signal;
KW Multigene family.
FT SIGNAL 1 32 POTENTIAL.
FT CHAIN 33 912 METABOTROPIC GLUTAMATE RECEPTOR 4.
FT DOMAIN 33 587 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 588 610 I (POTENTIAL).
FT DOMAIN 611 624 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 625 645 II (POTENTIAL).
FT DOMAIN 646 656 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 657 675 III (POTENTIAL).
FT DOMAIN 676 699 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 700 720 IV (POTENTIAL).
FT DOMAIN 721 750 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 751 772 V (POTENTIAL).
FT DOMAIN 773 785 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 786 808 VI (POTENTIAL).
FT DOMAIN 809 821 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 822 847 VII (POTENTIAL).
FT DOMAIN 848 912 CYTOPLASMIC (POTENTIAL).
FT CARBOHYD 98 98 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 301 301 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 454 454 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 484 484 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 569 569 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CONFLICT 124 124 Q -> R (IN REF. 2).
SQ SEQUENCE 912 AA; 101818 MW; 336430E19B4B577 CRC64;

Query Match 8.2%; Score 356.5; DB 1; Length 912;
Best Local Similarity 18.9%; Pred. No. 2.8e-19;
Matches 177; Conservative 164; Mismatches 374; Indels 221; Gaps 36;

QY 5 MTSDBGAVTFW--IFLLCLIAS-----PHLQGVAGRP-----DELHTGGIFPIAGK 48
Db 1 MSGKGWAWWARRPLCLLLSLYAPWVPSILGKPKGPHMNSIRIDGDTLGLGFPVHGR 60
QY 49 GHWQGGQAC-----MPATRLADDVKNOPNLLPGFKL----- 80
Db 61 G--SEGKACGELKKEGIHRLKLEAMLFALDRINNDPDLNITLGLARILDTCSRTHALEQ 118
QY 81 -----ILHSNDECEPGLGASVWYLLNYPKPKMLLAGC--STVCTTVAEAKKWNL 131
Db 119 SLTFVQALIEKDTGTEVRCGGGP-----ITKPERVGVGVIGAGSSVSIMVANILRFKI 174
QY 132 IVLCYGAASSPALSDRKRPFTLFRTHPSATVNPTRIKLMKFGWSRVAIL-----QQA 184
Db 175 PQISYASTAPDLSDNSRYDFFSRVVPSDTYQAQAMVDIVRAIKWNYVSTLASESGYGESG 234
QY 185 EEVFISTVEDLENRCMBAGVEIVTQSFSLSDPTDAVRNLRDRAIIVGLFYVVAARVL 244

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Qy	211	SFLSDPTDA-----VNNLRQDARIIVGLFVYVVAARVLCEMYKOOLYGRAHVWFFIGW	261
Db	252	KIPREPGPEFEKIIKRLLETPNARAVI-MFANEDDTIGILEAAKLNOSGHFLW--IG-	307
Qy	265	YEDNW-----YEVNLKAEIGTCTVEOMIAAEG---HLTTEALMNQNN---QTTIS	310
Db	308	-SDSWGSKIAPVYOEEIAEG-AVTILPKRASIDGDFRSTLANNRKNVWFAFSEG	365
Qy	311	GMTAEFERHRLNQALIEEGYDINHDPYEGYQE---APLAYDAVWSVALAFNKTMERLTT	367
Db	366	NFGCKSGSHGRNSHIKKCTGLERARIDSSYEGBGKVQFVIDAVSWAYALHNHMKELCP	425
Qy	368	GKKSLL--RDFTYTDKEIADEIYAAMNSTQFLGVSGV-VAFSSOGDRIALTQIBQ-MIDGK	423
Db	426	GYIGLCPRMWTIDGKELLYIRA---VNFNGSAGTPVTTFNENGDAAPGRYDIFQYI0NNK	481
Qy	424	--YEKLYGYDTOL----DNLSWLNTEQ-----WIGGR-449	
Db	482	STEYKIIGHWTNQLHVKEDQMANREHTHPASVCSLPCKPGKERKKTVGVPCCWCHGRC	541
Qy	450	-----VPODRITVTHVLRT-----VSL-----PLFVCMCTIISCCGFIVAF	484
Db	542	EGYNQVDELSCELCPLDOR--PNINRTGQORPIIKLEHHSWAVVPLVILAILGIATIT	599
Qy	485	ALIITFNWNKHRRVIOQSHPVCMNTIMLFGVVICLSVILIGIDGRFVSPPEYPKICQARA	544
Db	600	FVIVTFVRYNDTPIVRASGRELSVLLTIGIFLCYSITFLM-----TAAPTI--ICSFRR	652
Qy	545	WLLSTGFTLAYGAMFSKVRVHRFTTKAK---TDPKKKVEPKWLYTWVSGLLSIDVLILL	601
Db	653	IFLGLGCMFSAALLTKTNRIHRIFEGQKKSVPAP-KFTSPASQLVITTFSLISVQLLVGF	711
Qy	602	SWQIFDP---LQRYLETFFLEDPVSTDDIKIRPELEHESORNSMWLGLVYGFKGLILV	658
Db	712	VWVVDPPHIIDYGEQRTL-DPENARGVLK-----CDISDLSLCSL--GYSILLMW	761
Qy	659	FGLFLAYETRSIKVKQINDSRVYGMYSIYNNVVVLCILITAPVGMVIAQQDASF---AFVAL	715
Db	762	TCTVIAIKTRGVP-ETENEAKPIGFTMYTTCIIWLAFIPIFFCTAQSAEKMWIQTITTLV	820
Qy	716	AVIFCCFLMILLIFVPKIVIEVIRHPKDKAESKNYPOSATISKEDEERYQKLYTENEOQLRL	775
Db	821	SMLSASVSIGMLYMPKVYIIIFHPONVOKR-----KRSFKAVVTAATMQSKL	869
Qy	776	ITQKEERIRVLRLQRLVRBGRDAKGTGLNGATGVASAAVATTOPASLINGSAHA	828
Db	870	IQKNDR-----PNGEVK-SEL-----CESLETNTSSKTKTYISYSDHS	907
RESULT 11			
MGR7_HUMAN			
ID	MGR7_HUMAN	STANDARD;	PT; 915 AA.
AC	Q14831;		
DT	01-NOV-1997 (Rel. 35, Created)		
DT	01-NOV-1997 (Rel. 35, Last sequence update)		
DT	20-AUG-2001 (Rel. 40, Last annotation update)		
DE	METABOTROPIC GLUTAMATE RECEPTOR 7 PRECURSOR.		
GN	GM7 OR GPRC1G OR MGLUR7.		
OS	Homo sapiens (human).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
ON	NCBI_TaxID=9606;		
OX	[1]		
RP	SEQUENCE FROM N.A.		
RC	TISSUE=Brain;		
RX	MEDLINE=96437220; PubMed=8840028;		
RT	Makoff A., Pilling C., Harrington K., Emson P.;		
RT	"Human metabotropic glutamate receptor type 7: molecular cloning and		
RL	mRNA distribution in the CNS."		
RL	Brain Res. Mol. Brain Res. 40:165-170(1996).		
RN	[2]		
RX	SEQUENCE FROM N.A.		
RX	MEDLINE=98141892; PubMed=9473604;		

[illegible]

Qy 17 LLCLIA-----SPH---LOGGVAGRDELHIGGIFPIAGKGGWGGQAC-----57

FT DOMAIN 611 624 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 625 645 II (POTENTIAL).
FT DOMAIN 646 656 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 657 675 III (POTENTIAL).
FT DOMAIN 676 699 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 700 720 IV (POTENTIAL).
FT DOMAIN 721 750 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 751 772 V (POTENTIAL).
FT DOMAIN 773 785 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 786 808 VI (POTENTIAL).
FT DOMAIN 809 821 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 822 847 VII (POTENTIAL).
FT DOMAIN 848 912 CYTOPLASMIC (POTENTIAL).
FT CARBOHYD 98 98 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 301 301 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 454 454 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 484 484 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 569 569 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 912 AA; 101867 MW; 4A2F36E63A2EAF5A CRC64;

Query Match 8.1%; Score 353; DB I; Length 912;
Best Local Similarity 18.5%; Pred. No. 5.2e-19;
Matches 169; Conservative 179; Mismatches 371; Indels 196; Gaps 38;

QY I3 FWIPL-ICLIAS-----PHLOGGVAGRP-----DELHIGGIFPIAGKGGWGGQAC 57
DB I0 WVARLPCLLLSLXGPMWPSLGRPKGPHMNSIRIDGDTITGLGFPVHGRG--SEGKPC 67
QY 58 -----MPATRLADVDNKPQNLPGFKL-----IL 82
DB 68 GELKKEGIHRELAWLFDLRINDPDLNITLGLARILDCRSDTHALEOSLTFVQALI 127
QY 83 HSNDSCEPGLGASVMYNNLYNKPQKMLLAGC--STVCTTVAEAAKMWNLVLCYGASS 140
DB I28 EKDTEVRCGGGPP-----IITKERVVGVIGASGVSVIMVANILRLEKIPQISYASTA 183
QY I41 PALSDRKRFTPLFTHPSATVHNTPTRIKLMKFGWSRAIL-----QAAEEVFSTIVE 193
DB I84 POLSDNSRYDFFSRVWPSDTYQAQAMVDIVRAKWNVYSTVASEGSGYGEAFIQKSR 243
QY I94 DLENRCMEAGVEITROSFLSDPTDVRN-LRQDARIIVGLFYVVAARRVLCMEYKQOL 252
DB I24 EDGVCVTAQSVKI--PREPKAGEFDKIRRLLETNSARAVIIFANEDDIRRVLEAARRANQ 302
QY I25 YGRAHVWFFIGWYEDNW-----YEVNKAEG-ITCTVEQMRIAEGHLITTEALMWNQN 304
DB I303 TGH---FFWVG--SDSGSKTAPVHLHLEVAEGAVTILPKRMSVGRDPRYFSRRLDNNR 357
QY I305 NQTTSIGMTAEFRHLNQAALIEGYDI-----NHDTYPE--GYQE--APLAYDAVWSVA 355
DB I358 RNIWFAEFWEDNFHCKLSRHALKSGSHVKKCTNRERIGDSAYEQEGKVQFVIDAVYANG 417
QY I356 LAFNKTWERLTTGKSLRDTYTKETADEIYAAMNSTQFTLGVSG-VVAFSSQGD--RI 411
DB I418 HALHAMRDLCPGRVGL--CPRMDPVDGTQLLKLYIRNVNFSGIAGNPVTFNENGDPAGRY 475
QY I412 ALTOIEQIMID-GKYEKLG-----YDQTOLDNLSWLNTEQWIGKV-----PQDR----- 454
DB I476 DIYOYQLRNDSAEYKVGWTDHULHRIERHMHVPGSGQOLPRSCSLPCQPCGERKTKVKG 535
QY I455 -----TIVTHVLRT-----VSUPLFVC 471
DB I536 MPCWCHEPCTGYQYQVDRYTCPTCYDMRPTENTGCRPIPIKLEGSPWAVLPLFLA 595
QY I472 MCTISSCGIFVAFALIIFNIWNKHRRVIOSSHPPVCNTIMLFQVIFCLISVLLGIDGRFV 531
DB I596 VVGIAAT-LFWITFVRN-----DTPIVKASGRELSYVLLAGIFCYATTFLM-----IA 645
QY I532 SPEYPIKICQARWLLTGFTLAYGAMFSKVMVRVHRFTTKAK--TDPKKKVEPWKLYTMV 589
DB I646 EPD--LGTCSLRRIFLGLGMSISYAALLTKTNRIYRIFEQGRKRSVSAPRFISPSQLAIT 703

QY 590 SGLLSIDLVLISQWIFDPLQRYLETPELPDVPSTTDDIKIRPELHESQNSMMMLGLV 649
DB 704 FSLISQLIGICVFWFVVDPSHVVDD---FQD--QRTLDPRFARGVLKCDI--SOLSLICL 756
QY 650 YGFKGLILVEGLFLAYETRSIKVKQINDSRVYVGMISYNNVVLCLITAPVGMVIAQQDAS 709
DB 757 LGYSMLLVMTCTVVAIKTRGVP-ETFEAKPIGTTMTTCIVWLAFIPI--FFGTSQSD 813
QY 710 FAFV-----ALAVIFCFLSMLLIFVPKVIETVIRHPKDAESKYNPDSSAISKEDEERYQK 764
DB 814 KLYIQTTTLTVSVSLSASVSLGMLPKVYIILFHPQNPVKR-----KRSLK 861
QY 765 LVTENEQLQRLITQK 779
DB 862 AVVTAATMSNKFQK 876

RESULT I3
MGR7_RAT MGR7_RAT STANDARD; PRT; 915 AA.
AC P35400;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE METABOTROPIC GLUTAMATE RECEPTOR 7 PRECURSOR.
GN GRM7 OR GPRCIG OR MGLUR7.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=SPRAGUE-DAWLEY; TISSUE=Brain;
RX MEDLINE=94117433; PubMed=8288585;
RA Okamoto N., Hori S., Akazawa C., Hayashi Y., Shigemoto R.,
RA Mizuno N., Nakanishi S.;
RT "Molecular characterization of a new metabotropic glutamate receptor
mglur7 coupled to inhibitory cyclic AMP signal transduction.";
RL J. Biol. Chem. 269:1231-1236(1994).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=SPRAGUE-DAWLEY; TISSUE=Olfactory bulb;
RX MEDLINE=94195260; PubMed=8145723;
RA Saugstad J.A., Kinzie J.M., Mulvihill E.R., Segerson T.P.,
RA Westbrook G.L.;
RT "Cloning and expression of a new member of the L-2-amino-4-
phosphonobutyric acid-sensitive class of metabotropic glutamate
receptors.";
RL Mol. Pharmacol. 45:367-372(1994).
CC -!- FUNCTION: RECEPTOR FOR GLUTAMATE. THE ACTIVITY OF THIS RECEPTOR
IS MEDIATED BY A G-PROTEIN THAT INHIBITS ADENYLATE CYCLASE
ACTIVITY.
CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC -!- TISSUE SPECIFICITY: WIDELY DISTRIBUTED THROUGHOUT THE BRAIN.
CC -!- SIMILARITY: BELONGS TO FAMILY 3 OF G-PROTEIN COUPLED RECEPTORS.
CC STRONGEST, TO MGLUR4.
CC
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or send an email to license@isb-sib.ch).
CC
CC EMBL; D16817; BAA04092.1; -
DR EMBL; U06832; AAA20655.1; -
DR GCRDB; GCR_0945; -
DR GCRDB; GCR_0946; -
DR InterPro; IPR001828; ANF_receptor.
DR InterPro; IPR000337; GPCR_Mgr.
DR Pfam; PF00003; 7tm_3; I.
DR Pfam; PF01094; ANF_receptor; I.

DR EMBL: D13963; BAA03066.1; -
DR PIR: A46742; A46742.
DR GCRDB; GCR_0623;
DR InterPro; IPR001828; ANF_receptor.
DR InterPro; IPR000337; GPCR_Mgr.
DR Pfam; PF00003; 7tm_3; 1.
DR Pfam; PF01094; ANF_receptor; 1.
DR PRINTS; PR00248; GPCRMR.
DR PRINTS; PR00593; MTABOTROPICR.
DR PRINTS; PR01056; MTABOTROPICR.
DR PROSITE; PS00979; G_PROTEIN_RECP_F3_1; 1.
DR PROSITE; PS00980; G_PROTEIN_RECP_F3_2; 1.
DR PROSITE; PS00981; G_PROTEIN_RECP_F3_3; 1.
DR PROSITE; PS00982; G_PROTEIN_RECP_F3_4; 1.
DR PROSITE; PS0259; G_PROTEIN_RECP_F3_4; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein; Signal;
KW Multigene family; Vision.
FT SIGNAL 1 18
FT CHAIN 19 871
FT DOMAIN 19 579
FT TRANSSEM 580 602
FT DOMAIN 603 616
FT TRANSSEM 617 637
FT DOMAIN 638 648
FT TRANSSEM 649 667
FT DOMAIN 668 691
FT TRANSSEM 692 712
FT DOMAIN 713 742
FT TRANSSEM 743 764
FT DOMAIN 765 777
FT TRANSSEM 778 800
FT DOMAIN 801 813
FT TRANSSEM 814 839
FT DOMAIN 840 871
FT CARBOHYD 290 290
FT CARBOHYD 445 445
FT CARBOHYD 473 473
FT CARBOHYD 561 561
SQ SEQUENCE 871 AA; 95089 MW; 9F70B4D6A13B186D CRC64;

Query Match 7.6%; Score 334.5; DB 1; Length 871;
Best Local Similarity 20.3%; Pred. No. 1.3e-17;
Matches 180; Conservative 158; Mismatches 350; Indels 199; Gaps 39;

QY 11 VTFWIF---LLCLTASPHLQGVAGRPDLEHTIGFPIAGKGGWGGQAC----- 57
DB 11 LAWLWSQAGIACGAGSVRLAGG-----LTGLGLFPVHARGA--AGRACGALKKEQGVH 61

QY 58 -MPATRIALDDVNKOPNLLPGFKLLIHSNDSECE-----PGLGA 95
DB 62 RLEAMLYALDRVNADPELLPGVRLGARLDT-CSRDYALEQALSFPVQALIRGRGDGEA 120

QY 96 SV-----MYNLLYNKPKMLLAG--CSNVCTTVAEAKMNLVILVCYCASSPALSDDR 148
DB 121 SVRCPGGVPPURSPAPKRVAVGVASSVSVMVANVLRFAPQISYASTAPELSDSTR 180

QY 149 PPTLFRTPSATVNPTRIKMLKFGSRVALI-----QCAEEVFISTVELENRCME 201
DB 181 YDFSRVVPDSYQAQAMDIVRALGNVYVSLASEGNGVSGVFAFVQISREAGGVCTA 240

QY 202 AGVEIVTRQSFSDPTDAVRNLR---QDARIIVGLFFVVAARRVLCYEMKQOOLYGRAH 257
DB 241 QSIKIPREPCK---PGEPHKIVIRRLMETPNARGIIFANEDDIRRVLEATRQANLTGH-- 294

QY 258 VWFFIGHYEDNWE-----VNLKAGGI-TCIVQEQRIAAEG---HUTTEALMWNQNNQTT 308
DB 295 -FLWVG--SDSWGSKISPLNLEEEAVGAITILPKRASIDGDFQFMTSL---ENNRRN 348

QY 309 ISGMTAEFERRLNQAILECYD-----INHDYPEGVQEAPLAYDAVWSVA 355
DB 349 I--WFAEFWENFNCKLTSSGGQSDSTRKCTGEBRIGDSAYEKGKQVQFVIDAVIATA 406

QY 356 LAFNKTMERLTTGKKSLL-RDFTYTDKEIADEIYAAMNSTQFLGSGV-VAFSSQGD---R 410

DB 407 HALHSMHQAICPGHTGLCPAMEPTD---GRILLHVIKAVRFNGSAGTVPWFNENGDAQCR 463
QY 411 IALTQIE---QIMIDGKYEKLYG--DPQLDNLSWLNTQEWIGG--KVPQDRTIV----- 457
DB 464 YDIFOYQATNGSASSGGYQAVQMAEALRLD---MEVLRWSGDPHEVPPSQCSLPCGPG 519
QY 458 -----THVLR-TVSLPL 468
DB 520 ERKKNVKGVPCCWHCEACDGYRFQVDEFTCEACPDGDMRPTPNHTGCRPTPVVRLTWSSPW 579
QY 469 FVCMCTSSCGIFVAFALIIENINKNHRRVIOSSHPCVNTIMLFGV-IICLSVILLGID 527
DB 580 AALPELLAVLIGMATTTIMATFMHNDTPIVRASGRELSYVLLTGIFLYAIFLMAV-- 637
QY 528 GRFVSPEYPRKICQARAWLLSTGFTLAYGAFMSKVRVHRFTTKAK--TDRPKKVEPMKL 585
DB 638 -----EPCAICAARLLLGITLTSYALLTKTNIRYIFEQCKRSVTPPPFISPTSQ 691
QY 586 YTMVSGLLSIDLVILLWSQIFDPLQRYLETPLDPVSTTDDIKIRPELEHGESORNSMW 645
DB 692 LVITFGLTSLQVGVIAMLGAQPPHSVID---YEQRTVDPEQARGVLK-CDMSDLSL- 745
QY 646 LGLVYGFKGLLIVFGLFLAYETRSIKVKQINDSRVGVHSIYNNVLCILITAPGVNVIASQ 705
DB 746 IGCL-GYSLLLMVTCTVYAIKARGVP-ETFNKAPIGFTMYTTCIILAFVPI--FFGTA 801
QY 706 QDASFAFV-----ALAVIFCCFLSMILFVPKVIEVIRHPKDKAESK 747
DB 802 QSAEKIIQTTLIVSLSLASVSGLMLYVPKTYVILFHPHQNVQKR 848

RESULT 15
MGR3 RAT STANDARD; PRT; 879 AA.
AC P31422; 1993 (Rel. 26, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE METABOTROPIC GLUTAMATE RECEPTOR 3 PRECURSOR.
GN GRM3 OR GPRC1C OR MGLUR3.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=101116;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=921110002; PubMed=1309649;
RA Tanabe Y., Masu M., Ishii T., Shigemoto R., Nakanishi S.;
RT "A family of metabotropic glutamate receptors.";
RL Neuron 8:169-179(1992).
CC -!- FUNCTION: RECEPTOR FOR GLUTAMATE. THE ACTIVITY OF THIS RECEPTOR
CC IS MEDIATED BY A G-PROTEIN THAT INHIBITS ADENYLATE CYCLASE
CC ACTIVITY.
CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC -!- TISSUE SPECIFICITY: IS WIDELY DISTRIBUTED IN THE CNS. PREDOMINANT
CC EXPRESSION IS SEEN IN THE NEURONAL CELLS OF THE CEREBRAL CORTEX,
CC DENTATE GYRUS, AND GLIAL CELLS THROUGHOUT BRAIN REGIONS.
CC -!- SIMILARITY: BELONGS TO FAMILY 3 OF G-PROTEIN COUPLED RECEPTORS.
CC STRONGEST, TO MGLUR2.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (see <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC
CC EMBL; M92076; -; NOT_ANNOTATED_CDS.
DR PIR; JH0562; JH0562.
DR GCRDB; GCR_0362; -.

```
DR InterPro: IPR001828; ANF_receptor.
DR InterPro: IPR000337; GPCR_Mgr.
DR Pfam: PF00003; 7tm_3; 1.
DR Pfam: PF01094; ANF_receptor; 1.
DR PRINTS: PR00248; GPCRMR.
DR PRINTS: PR00593; MTABOTROPICR.
DR PRINTS: PR01053; MTABOTROPICR.
DR PROSITE: PS00979; G_PROTEIN_RECEP_F3_1; 1.
DR PROSITE: PS00980; G_PROTEIN_RECEP_F3_2; 1.
DR PROSITE: PS00981; G_PROTEIN_RECEP_F3_3; 1.
DR PROSITE: PS02059; G_PROTEIN_RECEP_F3_4; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein; Signal;
KW Multigene family.
FT SIGNAL 1 22
FT CHAIN 23 879
FT DOMAIN 23 576 METABOTROPIC GLUTAMATE RECEPTOR 3.
FT TRANSMEM 577 599 EXTRACELLULAR (POTENTIAL).
FT DOMAIN 600 613 I (POTENTIAL).
FT TRANSMEM 614 634 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 635 645 II (POTENTIAL).
FT TRANSMEM 646 664 EXTRACELLULAR (POTENTIAL).
FT DOMAIN 665 688 III (POTENTIAL).
FT TRANSMEM 689 709 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 710 734 IV (POTENTIAL).
FT TRANSMEM 735 756 EXTRACELLULAR (POTENTIAL).
FT DOMAIN 757 769 V (POTENTIAL).
FT TRANSMEM 770 792 VI (POTENTIAL).
FT DOMAIN 793 802 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 803 828 VII (POTENTIAL).
FT DOMAIN 829 879 CYTOPLASMIC (POTENTIAL).
FT CARBOHYD 209 209 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 292 292 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 414 414 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 439 439 N-LINKED (GLCNAC. .) (POTENTIAL).
SQ SEQUENCE 879 AA; 98959 MW; 3E5965EDD5E6DEED CRC64;
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Query Match 7.6%; Score 333; DB 1; Length 879;

Best Local Similarity 20.6%; Pred. No. 1.7e-17;

Matches 180; Conservative 132; Mismatches 313; Indels 250; Gaps 39;

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QY 36 ELHIGGIEPIAGKGGWGOAC-----MPATRLALDDVNKOPNLLPGFKLILHS 84
DB 38 DLVLGLGLFPINEKG---TGTECGRINEDRGIOQLKLEAMLFIDEINKDNYLLPGVKLGVI 95
QY 85 NDS-----ECEPGLGASVMYNNLYNKKPKMLLAGC-- 115
DB 96 LDTCSDRTYALQSLFVFRASLTKVDEAYMCPDG-----SYAIQENIP---LLIAGVIG 147
QY 116 ---STVCTTVAAAKMNNILVLCYGASSPALSDRKRPFTLFRTHPSATVHNPTRIKLMKK 172
DB 148 GSYSSVSQVANLLRLFQIPQISYASTSAKLSKSDRYDFARTVPPDFYQAKAMAEILRF 207
QY 173 FCWSRAVILQOAEVEFISTVEDE-----NRCMEAGVELVTRQSLDPTDAVRN-LRR 225
DB 208 FNMTYVSTVASEGDYGETGIEAFEQEARLNICI-ATAEKVGRSNIRKSYDSVIRELLQK 266
QY 226 ODARIIVGLF-----YVWAARRVLCEMYKQLYGRAHVWFFIGWYEDNWEVNLKAE 277
DB 267 PNARVVV-LFMRSDSRELIAANRV-----NASFTWV---ASDCWG-----AQE 307
QY 278 GITCTVEQMR IAAEGHLLTTEAL-----MWNQNNQNTTIS 310
DB 308 SI---VKGEHVAYGAITLELASHPVQFDRYFQSLNPNYNNHNPWFDPWEQKFCQSLQ 364
QY 311 GMTAEFRHLNQAILEEGYDINHRYPEGYQAPLAY--DAVMSVALAPNKTWERLTTC 368
DB 365 -----NKRNRHQVCKHLAIDSSNVE---QESKIMFVVVNAVYAMAHALHKMQRTLCPN 414
QY 369 KKSRLDF--TYTDKEIADFIYAAMNSTQFL---GYSVGVVAFSSQGDRIALTOI--EOMI 420
DB 415 TTKLCDAMKILDGKLYKLLKINFTAPFPNPKGADSIYKFDFTFGDGMGRYVFNLIQOT 474
```

```
QY 421 DGKYE--KLGYY-----DTOLDNLSW-----LNTEQ-----WI----- 446
DB 475 GGKYSYLVKGHWAETLSLDVDSIHMSRNSVPTSOCSDPCAENMKNMOPGDVCCWICIPC 534
QY 447 -----GKVP-----QDRTIVTHVLTVSLPLFVCMC 473
DB 535 EPVEYLDEFTCMDCGPGOWPTADLSGCYNLPEDYIKWEDAWAIGPV--TIACLGFLCTC 592
QY 474 TISSCGIFAFALIIFNINWKHRR---VIOSSHVPVCNTIMLFGVIICILISVILLGIDGRF 530
DB 593 -----IVITVFIKHNNTPLVKASGRELC-YILLFGVSLSYCMTF-----F 631
QY 531 VSPEEYKICOARAWLLSTGFTLAYGAMFSKVRVHRETTAKTDPK--KKVEPKLYTM 588
DB 632 FIAKPSPVICALRRLLGLTSPAICYALLTKNCIARIFDGVKNGAQRPKFISSSQVFI 691
QY 589 VSGLLSIDLVILLSQWIFDP--LQRYLETFPLEDPVSTDDIKIRPELEHCEQSQRNML 646
DB 692 CLGLILVQIVMVSVMWLLILETPGTRY--TLP-----EKRETVILKCNVKDSSMLI 739
QY 647 GLVYGFKGLILVFLGLFAYETRSIKVKOINDSRVGMISYNNVVLCLITAPVGMVIAQQ 706
DB 740 SLTYDV--VLVILCTVYAFKTRKCP-ENFNEAKFTGFTMTYTCIIWLAFLPFIYVYSSDY 796
QY 707 DASFAFVALAVIFCCFLSMLLIFVPKVIETIRHPK 741
DB 797 RVOTTTMCISVSLSGFVVVLGCLFAPKVHIVLFPOQ 831
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Search completed: April 30, 2002, 10:16:52

Job time: 224 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: April 30, 2002, 10:11:13 ; Search time 21 Seconds
(without alignments)
3046.982 Million cell updates/sec

Title: US-09-715-962-2
Perfect score: 4374
Sequence: 1 MRKDMTSDGAVTFWIFLLCL.....LINSSAHATPAATLAITQGE 840

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 219241 seqs, 76174552 residues
Total number of hits satisfying chosen parameters: 219241

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR.68:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	2024.5	46.3	960	2 JE0356	gamma-aminobutyric
2	457	10.4	402	2 T29703	hypothetical prote
3	356.5	8.2	912	2 JH0563	metabotropic gluta
4	355	8.1	908	2 I49142	metabotropic gluta
5	353	8.1	915	2 A49874	metabotropic gluta
6	342	7.8	879	2 JC7160	metabotropic gluta
7	334.5	7.6	871	2 A46742	metabotropic gluta
8	333	7.6	879	2 JH0562	metabotropic gluta
9	318	7.3	872	2 JH0561	metabotropic gluta
10	303.5	6.9	1171	2 A42916	metabotropic gluta
11	303	6.9	1218	2 S71376	glutamate receptor
12	302.5	6.9	1180	2 JC2132	metabotropic gluta
13	297.5	6.8	1212	2 JC2131	metabotropic gluta
14	294	6.7	999	2 T27628	hypothetical prote
15	268	6.1	1199	2 A41939	G protein-coupled
16	232.5	5.3	976	2 T51137	ionotropic glutama
17	219.5	5.0	1078	2 A56715	calcium receptor (
18	219	5.0	941	2 T51135	ligand-gated chann
19	213.5	4.9	1088	2 B56715	calcium receptor (
20	212.5	4.9	1079	2 I59362	calcium/polyvalent
21	212	4.8	1267	2 T21340	hypothetical prote
22	211.5	4.8	925	2 T06128	hypothetical prote
23	211.5	4.8	962	2 D86186	hypothetical prote
24	201.5	4.6	912	2 T51131	ligand gated chann
25	198.5	4.5	1085	2 S40476	Ca(2+)-sensing rec
26	193.5	4.4	551	2 T30806	metabotropic gluta
27	190.5	4.4	923	2 F84732	probable ligand-ga
28	189.5	4.3	953	2 E84732	probable ligand-ga
29	187	4.3	502	2 S69331	natriuretic peptid

RESULT 1
JE0356
gamma-aminobutyric acid receptor B precursor - human
N:Alternate names: GABA(B) receptor
C:Species: Homo sapiens (man)
C:Date: 05-Feb-1999 #sequence_revision 05-Feb-1999 #text_change 12-Feb-1999
R:Grifa, A.; Totaro, A.; Rommens, J.M.; Carella, M.; Roetto, A.; Borgato, L.; Zelante
Biochem. Biophys. Res. Commun. 250, 240-245, 1998
A:Title: GABA (gamma-amino-butyric acid) neurotransmission: Identification and fine m
A:Reference number: JE0356; MUID:98440782
A:Accession: JE0356
A:Molecule type: mRNA
A:Residues: 1-960 <GRI>
A:Cross-references: GB:Y11044; NID:g2826760
A:Note: this ORF is not annotated in GenBank entry HSGTHLAL, release 109
C:Genetics:
A:Map position: 6p21.3-6p21.3
C:Keywords: glycoprotein; neurotransmitter receptor; transmembrane protein
F:1-11/Domain: signal sequence #status predicted <SIG>
F:12-960/Product: gamma-aminobutyric acid receptor B #status predicted <MAT>
F:590-613/Domain: transmembrane #status predicted <TM1>
F:627-654/Domain: transmembrane #status predicted <TM2>
F:666-687/Domain: transmembrane #status predicted <TM3>
F:709-730/Domain: transmembrane #status predicted <TM4>
F:767-788/Domain: transmembrane #status predicted <TM5>
F:803-825/Domain: transmembrane #status predicted <TM6>
F:831-856/Domain: transmembrane #status predicted <TM7>
F:23,83,439,481,501,513,630/Binding site: carbohydrate (Asn) (covalent) #status predi

Query Match 46.3%; Score 2024.5; DB 2; Length 960;
Best Local Similarity 49.4%; Pred. No. 1.8e-149;
Matches 385; Conservative 151; Mismatches 220; Indels 23; Gaps 9;

Qy	24	PHLOGGVAGRPDE--LHTGGIFPTAGKGGGQACMPATRLALDDVNKPNLPGLKLI 81
Db	154	PHCVNTRPHSERAVYIGALFPMSS--GGWGGGQACQFAVENALEDVNSRRDILDPYELK 211
Qy	82	LHNSDSECEPGIGASVMYNLLYNKPQKMLLAGCSTVCTTVAEAAKMMNLIYLCYGASSP 141
Db	212	LHHDSKCDPCQATKYLYELLYNDPIKILMPGCSVSTLVAEARMNLIYLVSGSSP 271
Qy	142	ALSDRKRPPTLFRPHSPATVINPTRIKLMKFGWSRVAILQQAEEVFISTVEDLENRME 201
Db	272	ALSNRQRFPPTFFRTHPSATLHNPTRVKLFKMGWKKIATIQOTTTEVFTSTLDLEERVEK 331
Qy	202	AGVEIVTRQSFSLSDPTDAVRLNRDADRIIVGLFYVAARRVLCVMYKQOLYGRAHVWF 261
Db	332	AGIEITFRQSFSDPAVPVKNLKRQDARIIVGLFYETEARKVFCVEYKERLGRKYVWFL 391
Qy	262	IGWYEDNMYEVNLKAEGITCTVEQMR IAAEGHLTTAALMWNQNNQTTISGMTAEFRHL 321

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Db 392 IGVYADNWFKI--YDSINCTVDMEAEVGHITTEIVMLNPNANTRISISNMTSQEFVEKL 449
QY 322 NQALIEEGYDINHRYPE---GYQEAFLYDAVMSVALAFNKTMRLETTTGKKSRLDFTYT 378
Db 450 TKRL-----KRHEETGGFOEAPLAYDAIWAALALANKTSGGGRSVRLEDNFYN 500
QY 379 DKEIADEIYAAMNSTQFLGVGVVAFSSQGDRIALTOIEQMIDGKYEKLGYDYDQLDNLS 438
Db 501 NQITDQIYRAMNSSFEVSGVHVFDASGRMAWTLIEQPQGSYKKIGYDSTKDDLS 560
QY 439 WLNTQEWIGKVPQDRTIVHRTVSLPLFCVCMCTISSCGIFVAFALIIFNIWKKHRRV 498
Db 561 WSKTDKWIGSPADQTLVTKTRFSLQKLFISVSLSSUGLIVAVCLVSNFIYNSHVRY 620
QY 499 IQSSHVPVCNTIMLFVGIICILSIVLLIGIDGRFVSPPEYPRKICQARAWLLSTGFTLAYGAM 558
Db 621 IQNSQPNLNLTAVGCSLAAVFPGLDGYHGRNQFPFVCQARLWLLGLGFSGLVGS 680
QY 559 FSKVWRVHR-FTTK-AKTDPKKKVPMKLYTMVSGLLSIDLVILLSSQIFDPLQRYLET 616
Db -681 FTKIWWVHTGFTKKEKKEWRKTLKPWKLYATVGLLVGMDVLTALWQIVDPLHRTIET 740
QY 617 PLEDPVSTDDIKIRPELEHCEQSQRNSMWGLVYGFKGLILVFGFLAYETRSIKVKQIN 676
Db 741 AKPEEKEDI-DVSIPLQLEHCSRKNMTWLGIFYGKGLLLGIFLAYETKSVSTKIN 799
QY 677 DSRVYGMSTYNNVVVLCITAPGVMTASQODASFAFVALAVIFCCFLSMILLIFVPKIV 736
Db 800 DHRVAGMAYNNVAVLCITAPVMTILSSQODAAFAFASLAIIVFSSYITLVVLFVPMK 859
QY 737 IRHP--KDAESKYNPDSAISKEDERYQKLVTENEQRLITQKEEKIRVLRQRLVER 793
Db 860 ITRGEWQSEADQTMKTGSSNTNNEEKSRLLEKENRELEXIIAEKERVSELRLQLQSR 918

RESULT 2
T29703
hypothetical protein ZK180.1 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C:Accession: T29703
R:Pauley, A.; Le, T.T.
submitted to the EMBL Data Library, May 1996
A:Description: The sequence of C. elegans cosmid ZK180.
A:Reference number: Z20669
A:Accession: T29703
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-402 <PAU>
A:Cross-references: EMBL:U58748; PIDN:AA52965.1; GSPDB:GN00022; CESP:ZK180.1
A:Experimental source: strain Bristol N2; clone ZK180
C:Genetics:
A:Gene: CESP:ZK180.1
A:Map position: 4
A:Introns: 25/3; 98/2; 219/3; 253/3; 280/1; 309/1; 339/2; 357/3; 395/2

Query Match 10.4%; Score 457; DB 2; Length 402;
Best Local Similarity 29.9%; Pred. No. 1e-27;
Matches 132; Conservative 74; Mismatches 161; Indels 74; Gaps 15;

QY 389 AMNSTOFLGVGVVAFSSQGDRIALTOIEQMIDGKYEKLGYDYDQLDNLSLWN--TEQWI 446
Db 15 AINSSFOGLTGKVKFAN-NERGLVDIKQWSQGYVPFVAYGDADDEFKIIDSTTKGW- 72
QY 447 GKKVPQDRTIVHRTVSLPLFCVCMCTISSCGIFVAFALIIFNIWKKHRRVIOSSHVPC 506
Db 73 --SPPLDSTITERREHISILFLAM-----SLF-----IKMSSPNL 107
QY 507 NTMLFGVICTLSVILLGIDGRFVSPPEYPRKICQARAWLLSTGFTLAYGAMFSKVRVH 566
Db 108 NNIIAGSICTFASVIMGLDTRIVSPDVFVWLCYTTKTWTLCIGTILSFGAMFSKTRVH 167
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QY 567 RFTTKAKTDPPKKVPMKLYTMVSGLLSIDLVILLSSQIFDPLQRYLETFFLEDVPSYTD 626
Db 168 SIFTNIRMD-BKAKDSKLFILGILLFDICVLVTWAFVSPFS-YTVT---ELPHIPED 222
QY 627 DIKTRPELEHCEQSQRNSMWGLVYGFKGLILVFGFLAYETRSIKVKQIINDSRVYGMSTY 686
Db 223 NIVIPEKEKNSSSGVGFQAVLYAVKGVLMILGFLAWETHRVNVPALNDSKIYIGTR-- 280
QY 687 NVVVLCLITAPVGMVIAISQODASFAFVALAVIFCCFL---SMLLIFVPRKVIIVIRHPKDK 743
Db 281 -----TCQRDVOSRFV-----FCHFLDDTNVVSRCADSKFSKTPNFI 319
QY 744 AESKYNPDSAISKED-----ERYQKLVTENEQRLITQKEEKIRVLRQRLVERGDAKGT 800
Db 320 MKLFFN-----ESKNSYGGFKNFQKLSFGGFNIVFARSQVKKKVIELARNPV-----GNE 369
QY 801 LNG-ATGVASRAVATTSPAS 820
Db 370 PRAYRRGLMKSVVAKTSQPM 390

RESULT 3
JH0563
metabotropic glutamate receptor 4 precursor - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 17-Nov-2000
C:Accession: JH0563; I58149
R:Tanabe, Y.; Masu, M.; Ishii, T.; Shigemoto, R.; Nakanishi, S.
Neuron 8, 169-179, 1992
A:Title: A family of metabotropic glutamate receptors.
A:Reference number: JH0561; MUID:92110002
A:Accession: JH0563
A:Molecule type: mRNA
A:Residues: 1-912 <TAN>
A:Experimental source: brain
R:O'Hara, P.J.; Sheppard, P.O.; Thøgersen, H.; Venezia, D.; Haldeman, B.A.; McGrane,
Neuron 11, 41-52, 1993
A:Title: The ligand-binding domain in metabotropic glutamate receptors is related to
A:Reference number: I58149; MUID:93332699
A:Accession: I58149
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-123,'R',125-912 <RES>
A:Cross-references: GB:M90518; NID:g205400; PIDN:AAA93190.1; PID:g205401
C:Comment: This protein is coupled to a G protein and evokes a variety of functions b
C:Genetics:
A:Gene: GLUR4
C:Superfamily: metabotropic glutamate receptor 4
C:Keywords: G protein-coupled receptor; glycoprotein; neurotransmitter receptor; phos
P:1-32/Domain: signal sequence #status predicted <SIG>
P:33-912/Product: metabotropic glutamate receptor 4 #status predicted <MET>
P:588-610/Domain: transmembrane #status predicted <TRI>
P:625-645/Domain: transmembrane #status predicted <TII>
P:657-675/Domain: transmembrane #status predicted <III>
P:700-720/Domain: transmembrane #status predicted <IV>
P:751-772/Domain: transmembrane #status predicted <TRV>
P:786-807/Domain: transmembrane #status predicted <TVI>
P:822-847/Domain: transmembrane #status predicted <VII>
P:98,301,454,484,569/Binding site: carbohydrate (Asn) (covalent) #status predicted
P:621,689,695,859,870/Binding site: phosphate (Ser) (covalent) #status predicted
```

```

Query Match 8.2%; Score 356.5; DB 2; Length 912;
Best Local Similarity 18.9%; Pred. No. 2.5e-19;
Matches 177; Conservative 164; Mismatches 374; Indels 221; Gaps 36;

QY 5 MTSDCAVTFW--IFLLCLIAS-----PHLQGVAGRP-----DELHIGGIPPIACK 48
Db 1 MSGKGGWAWWRLPCLLLSLIYAPVWPSLKGPKGPHMNSIRINDGDTITLGLFPVHR 60
QY 49 GQWQGGQAC-----MPATRLALDDVNRKPNLLPFGKLI----- 80
```

[illegible]

A;Cross-references: EMBL:U17252; NID:g854728; PIDN:AAA68149.1; PID:g854729
C;Genetics:
A;Gene: mGluR8
C;Superfamily: metabotropic glutamate receptor 4
C;Keywords: neurotransmitter receptor

Query Match	8.1%	Score 355;	DB 2;	Length 908;
Best Local Similarity	21.0%;	Pred. No. 3.3e-19;		
Matches	200;	Conservative 159;	Mismatches 390;	Indels 204; Gaps
Qy	13	FWIFLLCLIAAPHLOGGVAG-RPD-ELHIGGIPPIACKGMOGQOAC-----MP 59		
Db	22	YWI--LTMQTHSQEYAHSTRIGDDIILGGLFPVHAKG--ERGVPCCDLKKEGJHRL 77		
Qy	60	ATRIALDDVVKQPNLLPGFKL---IL-----HSNDSECEPGL 93		
Db	78	AMLYAIDQTKNDPOLLNSITLGVRILOTCSDRTYALBQSLTFVQALIEKDAQSVKCA 137		
Qy	94	GASVWYNLLYNKPKL--MLLAGCSTVCTVAAEAKMWNLLVLCYGASSPALSDRKEPT 151		
Db	138	PP-----IFTKPKISGVIAAASSVSLMVANILRLFKIPQISYASTABSDNTRYDF 191		
Qy	152	LFRTHPSATVHNPRIKLMKFGMSRAILQQAAEEVFISTVEDLENRCMP-AGVEIVTRQ 210		
Db	192	FSRVVPPDSYQAQAMVDIVTALGNVYSTLASEGNYCESGVEAFTQISREIGGVCAQ 251		
Qy	211	SFLSDPTDA-----VNLRRQDARIIVGLFVYVVAARRVLCEMYKOOLYGRAHWFFIGW 264		
Db	252	KIPREPRGPEFEKIIRKLETPNARAVI-MFANEDDIRGILEAAKLINQSGHFLW--IG- 307		
Qy	265	YEDNW-----YEVNLKAEIGITCTVEQMRIAABG---HLTTEALMNQNN---OTTIS 310		
Db	308	-SDWSGKIAPVYQOEETAEAG-AVTILPKRASIDGDPDFRSTLANNRRNVWFAESEG 365		
Qy	311	GMTAEFRHRLNQALIBEGYDINHDPYEGYQE---APLAYDAVWSVALAFNKTMRLETT 367		
Db	366	NFGCKSGSHGRNRRSHIKKCTGLERIASDSSYEQEGKVQFVIDAVYSMAYLHNHRELCP 425		
Qy	368	GKKSLL--RDTYTDKEADEIYAAMNSTQFLGVSGV-VAFSSOGDRIALTQIEQ-MIDGK 423		
Db	426	GYIGLCPRMWTIDGKELLYIRA---VNFNGSAGTPTVTENGDAPGRYDIFQYQNNK 481		
Qy	424	--YKELGYDTQL---DNLSWLNTEQ-----WIGGK-449		
Db	482	STEYKIIGHWTNQLHLKVEDQMWARREHTHPASVCSLPCKPGERKKTVKGPCWCHGRC 541		
Qy	450	-----VPQDRIIVHLVT-----VSL-----PLFCMCTLSGCGIFVAF 484		
Db	542	EGYNQVDELSCELCPLDQR--PNINRTGQORPIIKLEHWSWAVVPVLLIATLIATTT 599		
Qy	485	ALIIFNTWNKHRRVIQSSHPVCNTIMLFGVILICLISVILIGIDGRFVSPPEYKICQARA 544		
Db	600	FVIVTFVRYNDTPIVRASGRELSVLLTGIFLCYSITFLM-----IAAPDTI--ICSFR 652		
Qy	545	WLLSTGFTLAYGAMFSKWRVHRETTAK--TDPKKKVPWKLYTMWSGLLSIDLIVLL 601		
Db	653	IFLGLGCMFSYAAALLTNRHIFRFEQGGKSVTAP-KFISPASQVLITFSLISVQLLGWF 711		
Qy	602	SWQIFDP---LQRYLETFPLEDPVSTDDIKIRPELHCESQRNSMWGLGVYFGKGLIIV 658		
Db	712	WVFVVDPHPTIIDYGEORTL-DPENARGVLK-----CDISDLSLICSL--GYSILLMW 761		
Qy	659	FGLFLAYETRSIKVKQINDSRVGMSTYNNVVILCLITAPVGWVIASQODASF---AFVAL 715		
Db	762	TCTVVAIKTRGVP--ETNEAKPIGFTWYTCIIWLAFPIFFCTGAQSAEKMYIQTITTLAV 820		
Qy	716	AVIFCCFLSMILLFPVKVIEVIRHPKDKAESKYNPDSAISKDEERYOKLVTENEQQLRL 775		
Db	821	SMSLSASVSGLMTPKVVYIIIFHPEQNVQKR-----KRSEKAVVTAAATWQSKL 869		
Qy	776	ITQKEEKIRVLQRBLVERGDAKGTGELNAGTCVGSAAAVATTSQPASLINSASAH 828		

Db 870 IQKGNDR-----PNGEVK-SEL-----CESLETNTSSTKTTYISYSDHS 907

RESULT 5
A49874

metabotropic glutamate receptor 7 - rat
N:Alternate names: metabotropic glutamate receptor mGluR7
C:Species: Rattus norvegicus (Norway rat)
C>Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 24-Sep-1999
C:Accession: A49874; I57954
R:Okamoto, N.; Hori, S.; Akazawa, C.; Hayashi, Y.; Shigemoto, R.; Mizuno, N.; Nakanishi, J. Biol. Chem. 269, 1231-1236, 1994
A:Title: Molecular characterization of a new metabotropic glutamate receptor mGluR7 comp
A:Reference number: A49874; MUID:94117433
A:Accession: A49874
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-915 <RES>
A:Cross-references: GB:D16817; NID:9458728; PIDN:BAA04092.1; PID:g458729
R:Saugstad, J.A.; Kinzie, J.M.; Mulvihill, E.R.; Segerson, T.P.; Westbrook, G.L. Mol. Pharmacol. 45, 367-372, 1994
A:Title: Cloning and expression of a new member of the L-2-amino-4-phosphonobutyric acid
A:Reference number: I57954; MUID:94195260
A:Accession: I57954
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-915 <RE2>
A:Cross-references: EMBL:U06832; NID:g459657; PIDN:AAA20655.1; PID:g459658
C:Genetics:
A:Gene: MGLUR7
C:Superfamily: metabotropic glutamate receptor 4
C:Keywords: neurotransmitter receptor

Query Match 8.1%; Score 353; DB 2; Length 915;

Best Local Similarity 21.2%; Pred. No. 4.8e-19; Mismatches 320; Indels 290; Gaps 50;

Db 17 LLCLIA-----SPH-----LOGGVAGRPDELHIGGIFPIAGKGWGGQAC----- 57
Db 24 LLCVLAARAGQEMYPHSHRIEDVT-----LGGFLFPVHAKG--PSGVPCGDIKREN 74
Qy 58 ----MPATRLALDDVNKPNLLPGFKL--IL-----L-----HNSDS 87
Db 75 GHRLEAMLYALDQINSDPNLLPNVTLGARILDTCSRDTYALEQSLTFVQALIGKDTSDV 134
Qy 88 ECEPGLGASVMYLLYNKPKMLLAGC--STVCTTVAEAKWNVLVLCYGASSPALSD 145
Db 135 RCTNGEPP-----VFKPEKVVGVIGASGSSVIMVAVILRUFQIPQISYASTAPELSD 188
Qy 146 RKRFPFLFRTHPSATVHNPTRIKMKFGWSRVAILQQAEEVFSTVEDLENRCMEAGVE 205
Db 189 DRYDFFSRVVPDPSFQAQAMVDIVKALGN-----YVSTLAS-EGSGYGEKGE 236
Qy 206 IVTRQSFSLDPTDAVNRLR-----RQDA-----RIIVGLFVVAARRVLC-----EMYKOOL 252
Db 237 SFTQISKEAGGLCAQSVRIPOERKDRITDFRIIKOLLDTPNRSRAVVIFANDEDIKQIL 296
Qy 253 YG--RA-HWFFFGWYEDNW-----YEVNLAEGITCIVEQMRIAEG--HLTTEAL 299
Db 297 AAKRADQVGHFLWVGSDSMGSLNPLHQHEDIAEG-AITIQKRAVTEGFDVAFYFTRTL 355
Qy 300 -----MW-----NONNOTTISGMTAEF-RHRLNQAALIEGVDINHDYRPGYQEAP 345
Db 356 ENNRNVWFAEYEEFNPKLTISGSKEDTDRKCTQERI--GKDSNYEQ--EG--KVQ 409
Qy 346 LAYDAVMSVALAPNKTMRITLT-----GKKSRLDFTYTDKETADEIYAAMNS 392
Db 410 FVIDAVYAMAHALHNMKDLCADYRGVCPMEQAAGGKKLLKYIRHN----- 456
Qy 393 TQFLGVSQV-VAFSSQGDRTALQIEQMDCKVEKLYGYDTQLDNLSW-----L 440
Db 457 --FNGSAGTPVMENKNGD-----APGRYDIFQYQTTNTNPGYRLIGQWTDLEQL 504

Qy 441 NTE--QWITGG--KVPQ-----VSLPLFVCMCTISSCGIFVAFALIININKHRR 459
Db 505 NIEDMQMGKGVRETPSSVCTLPCKPQRKKTQKGTCCWTCPCDGYQYQFDEMTQCHCP 564
Qy 460 -----VLRT-----VLT-----VLT-----VLT-----DRTIVTH-- 459
Db 565 YDQRPENRTGCQNIPIIKLEWHSPWAVIPVFLAMLGIAT-IFVNATFIRYN---DTP 619
Qy 498 VIOSSHPCNTIMLFGVILICISVILLGIDGRFVSPEEYPKICQARAWLLSTGFTLAYGA 557
Db 620 IVRASGRELVSLLTGIFLCYIITFLM-----IAKPD--VAVCSFRFVLGCMCISAA 672
Qy 558 MFSKVMVRHRTTKAK---TDPKKKVEPKWLYTVMSGLSIDLVLLSQIDPLQRYLE 614
Db 673 LLTKTNRIYRIFEQCKKSVTAP-RLISPTSQLATSSILSVQLLGVFIWFGVDPPNIID 731
Qy 615 TFPLEDVSTDDIKIRPELEHCEQSQRSMWGLVYGFKGLLIVLGLFLAYETRSIKVKQ 674
Db 732 ----YDEHKTMPNQARGVLK-CDITDLQIICSL--GYSILLMVCTVYAIKTRGVP-EN 783
Qy 675 INDSRYGMSIYNVVVLCITAPVGMVITASQODASFAFV-----ALAVIFCCFLSMLLIF 729
Db 784 FNEAKPIGTMTTCIVWLAFIPI--FTGTAQSAEKLYIQTTTLTISMWLSASVALGM 841
Qy 730 VPKVIEVIRHPKDKAESKYNPDSAISKEDERYQKVLITENEQRLQRLITQKEEKIRVLR 789
Db 842 MPKVYIIIFHPELNVQKR-----KRSEKAVVTAATMSSRLSHKPSDR----- 883
Qy 790 LVERGDAKGTTEL 801
Db 884 --PNGEAK--TEL 892

RESULT 6

JC7160

metabotropic glutamate receptor subtype 3 precursor - mouse

C:Species: Mus musculus (house mouse)

C>Date: 04-Mar-2000 #sequence_revision 04-Mar-2000 #text_change 11-May-2000

C:Accession: JC7160

R:Minoshima, T.; Nakanishi, S.

J. Biochem. 126, 889-896, 1999

A:Title: Structural organization of the mouse metabotropic glutamate receptor subtype

A:Reference number: JC7160; MUID:20012997

A:Accession: JC7160

A:Molecule type: DNA

A:Residues: 1-879 <MIN>

A:Cross-references: GB:Afl70696

C:Genetics:

A:Gene: mGluR3

C:Superfamily: metabotropic glutamate receptor 4

C:Keywords: differentiation; G protein-coupled receptor; receptor; transmembrane prot

F:1-24/Domain: signal sequence #status predicted <SIG>

F:25-879/Product: metabotropic glutamate receptor subtype 3 #status predicted <TM1>

F:577-599/Domain: transmembrane #status predicted <TM2>

F:614-634/Domain: transmembrane #status predicted <TM3>

F:646-664/Domain: transmembrane #status predicted <TM4>

F:689-709/Domain: transmembrane #status predicted <TM5>

F:735-756/Domain: transmembrane #status predicted <TM6>

F:770-791/Domain: transmembrane #status predicted <TM6>

F:804-828/Domain: transmembrane #status predicted <TM7>

Query Match 7.8%; Score 342; DB 2; Length 879;

Best Local Similarity 20.5%; Pred. No. 3.2e-18;

Matches 182; Conservative 132; Mismatches 300; Indels 272; Gaps 41;

Qy 36 ELHIGGIPPIAGKGWGGQAC-----MPATRLALDDVNKPNLLPGFKLILHS 84

Db 38 DLVIGGLFPINEKG--TGTEECRGINEDRGIQRLAFLAIDEINKKNYLLFCVKGIVHI 95

Qy 85 NDS-----ECEPGLGASVMYLLYNKPKMLLAGC--- 115

Db 96 LDTCSRDYVALQSLFVFRASLTAKVDEAEYMCPCD-----SYAIQENIP-----LLIAGVIG 147

Qy 116 ---STVCTTVAEAAKMNLLIVLCYGASSPALSDDKRPFLFRTHPSATVNPTRIKLMKK 172

Db 148 GSYSSVSIQVALLRFQIPQISYASTAKLSKSDYDFARTPPDYQAKMAEILRY 207

Qy 173 FGWSRAIIQQAAEEFISVDELE-----NRCMEAGVEIVTRQSFSLDPTDAVRN-LRR 225

Db 208 FNTWTVSVASEGDTGETIEAFQEARLNICI-ATAEKVGRSNIRKSYSDSVIRELLQK 266

Qy 226 QDARIIVGLF-----YVVAARRVLCMEYKOOLYGRAHVVEFFIGWIEDNWTVEVNLKAE 277

Db 267 PNARVVV-LFMRSDDSRELLIAASRV-----NASFTWV-----ASDGVG-----AQE 307

Qy 278 GITCTVEQMRIAAGHLTTEAL-----MNQNNQNTTIS 310

Db 308 SI-----VKGSEHVAIGAITLEASHPVQRFDRYFQSLNPNYNNHNPWFDRDFWEQKFCQSLQ 364

Qy 311 GMTAEFRHLRNOALLEEGYDINHDIRYPEGYQEAPLAY--DAVWSVALAFNKTMERL--- 365

Db 365 -----NKRNRHQICDKHLAIDSSNYE---QESKIMFVVVNAVYAMAHALHMKORTLCPN 414

Qy 366 TT-----GKSLRDTFTYDKIEADIYAAMNSTOFLGVSVVAFSSQGDRIALTQ 415

Db 415 TTKLCDAMKILDKKLYDKYL-----LKNFTAPFPNPK--GADSIKFTDYGDGMGRYN 467

Qy 416 I---EQMIDGKYE--KLGYDYDTOL-----DNLSWLNTE----- 443

Db 468 VNFQHIGKYSYLVKGHWAETLYLDVDSIHWSRNSVPTSQSDCAPNEMKMQPGDVC 527

Qy 444 -----QW-----TGG--KVPQDRTIVTHVLR----- 462

Db 528 CWICIPCEPYEYLVDEFTCMCGPGQWPTADLSGCYNLPED-----YIRWEDAWAIGPV 581

Qy 463 TVSLPLFCVCMCTISSCGIFVAFALIIFNIWNKRR---VIOSSHVCNTIMLFGVILICLI 519

Db 582 TIACLGFMCTC-----IVITVIKHNWTPLVKASGRELC-YILLFGVLSYSC 627

Qy 520 SVILGIDGRFVSPEYPRKICQARAWLLSTGETLAYGAMFSKVMRVHRTTKATDPK-- 577

Db 628 MTF-----PFIAPKSPVICALRLRLGLGTSFAICYSAALLTKTNCIARIFDGVKNGAQR 680

Qy 578 KKVEPKLYTWVSGLLSIDLVLLSQIFDP--LQRYLETFFLEDVPVSTDDIKIRPELE 635

Db 681 KFISSPSSQVFICGLILVQIVMVSVWLIETPGTRRY--TLP-----EKRETVIL 728

Qy 636 HCESORNSMGLVGVGFKGLIIVGLFLAYETRSIKVKOINDSRVYGMSTYNNVVLCILIT 695

Db 729 KCVNDSSMLISLTIDV--VLVILCTVYAFKTKCP-ENFNEAKFIGFTMYTTCIIWLAF 785

Qy 696 APVGMVIAASQODASFAFVALAVIFCCFLSMILLIFVPKVEIVRHPK 741

Db 786 LPFVVTSSDYRVQVTTWICISVLSLGFVVLGCLFAPKVIHLVFPQ 831

RESULT 7

A46742

metabotropic glutamate receptor, mGluR6 - rat

C:Species: Rattus norvegicus (Norway rat)

C:Date: 21-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 20-Jun-2000

C:Accession: A46742

R:Nakajima, Y.; Iwakabe, H.; Akazawa, C.; Nawa, H.; Shigemoto, R.; Mizuno, N.; Nakanishi

J. Biol. Chem. 268, 11868-11873, 1993

A:Title: Molecular characterization of a novel retinal metabotropic glutamate receptor m

A:Reference number: A46742; MUID:93280152

A:Accession: A46742

A>Status: preliminary

A:Molecule type: nucleic acid

A:Residues: 1-871 <NAK>

A:Cross-references: GB:DL1363; NID:g391856; PIDN:BAA03066.1; PID:g391857

A:Experimental source: retina

A>Note: sequence extracted from NCBI backbone (NCBI:133246, NCBI:133250)

C:Superfamily: metabotropic glutamate receptor 4

C;Keywords: G protein-coupled receptor; transmembrane protein

Query Match 7.6%; Score 334.5; DB 2; Length 871;
Best Local Similarity 20.3%; Pred. NO.1.2e-17;
Matches 180; Conservative 158; Mismatches 350; Indels 199; Gaps 39;

Qy 11 VTFWIF---LCLTASPHLQGGVAGRPDELHIGGIFPTAGKGGWGGQAC----- 57

Db 11 LAWLMSQAGIACGAGSVRLAG-----LTLGLFPPVHARGA--AGRACGALKKEQGVH 61

Qy 58 -MPATRALDQVKNOPNLLPGFKLILHSNDSECE-----PGLGA 95

Db 62 RLEAWLVALDRVADPELLPGVRLGARLLDT--CSRDTVALEQALSFVQALIRGRGDGEA 120

Qy 96 SV-----MYNLLYNKPKQLMLIAG--CSTVCTTVAEAAKMNLLIVLCYGASSPALSDDKRR 148

Db 121 SVRCGGVPPLRSAPPERRVAVVGASASSVIMVANVLRFLFAIPQISYASTAPELSDSTR 180

Qy 149 PPTLFRTHPSATVNPTRIKLMKFGWSRAIL-----QQAEEVFISTVEDLENRME 201

Db 181 YDFESRVVPPDSYQAQAMVDIVRALGWNVYSTLASEGNYGESGVEAFVQISREAGGVCA 240

Qy 202 AGVELIVTRQSFSLDPTDAVRNLR---QDARIIVGLFVVAARRVLCMEYKOOLYGRAH 257

Db 241 QSIKIPREPK---PGEFHKVIIRLMETPNARGIILIFANEDDIRVLEATROANLTGH-- 294

Qy 258 VWFFIGWYEDNWYE-----VNLKAEGI--TCTVEQMRIAAG---HLTTEALMNQNNQNTT 308

Db 295 -FLWVG--SDSWGSKISPIILNEEAAGAITILPRASIDGFDQYFMTSL---ENNRN 348

Qy 309 ISGMTAEFRHLRNOALLEEGYD-----INHDYRPEGYQEAPLAYDAWSVA 355

Db 349 I--WFAEFWEENFNCKLTSSGQSDSTRKCTGEERIGODSAYEQEKVQVIFAAYAIA 406

Qy 356 LAFNKTHERLTTGKSL--RDTYTDKETADEIYAAMNSTOFLGVSGV-VAFSSQGD---R 410

Db 407 HALHSMHQALCPGHTGLCPAMEPTD---GRTLHLHIVRAVRFNAGSAGTVMFNENGDAFGR 463

Qy 411 IALTQIE---QIMDGKYEKLYG--DTQLDNLSLNTTEOWIGG--KVPQDRTIV----- 457

Db 464 YDIFQYQATNGSASSGGYQAVQWAEALRLD---MEVLRWSGDPHEVPPSQCSLPCGPG 519

Qy 458 -----THVLR-TVSLPL 468

Db 520 ERKKMWKGVPCCHCEACDGYRFQVDEFTCEACPGCDMRPTNHTGCRPTPVVRLTWSSPW 579

Qy 469 FVCMCTISSCGIFVAFALIIFNIWNKRRVITQSSHPVCNTIMLFGV-IICLISVILLGID 527

Db 580 AALPLLAVLIGIMATTTIMATFMRHNDTPIVRASGRELSYVLLTGIFLIYAITFLMVA-- 637

Qy 528 GRFVSPEYPRKICQARAWLLSTGETLAYGAMFSKVMRVHRTTKAK--TDPKKEVPWKL 585

Db 638 -----EPCAAICAARLLGLTSLTSALITKTNRIYRIFEQGRKSVTPPPFISPTSQ 691

Qy 586 YTMVSGLLSIDLVILLSMQIFDPLQRYLETFFLEDVPVSTDDIKIRPELEHCEQSRNSMW 645

Db 692 LVITFGLTSLQVGVVIAWLGAPPHSVID---YEEQRTVDPQEQARGVLK-CDMSDSL- 745

Qy 646 LGLVYGFGLIIVLPGFLAYETRSIKVKQINDSRVYGMSTYNNVVLCILITAPVGMVIAAQ 705

Db 746 IGCIL-GYSLLLMWCTVYVIAKARGVP-ETFEAKPIGFTMYTTCIIWLAFVPI--FFGTA 801

Qy 706 QDASFAFV---ALAVIFCCFLSMILLIFVPKVEIVRHPRDKAESK 747

Db 802 QSAEKIYIQTTLTIVSLSLASVSGLMGLYVPKTYVILFHPHONVQKR 848

RESULT 8

JH0562

metabotropic glutamate receptor 3 precursor - rat

C:Species: Rattus norvegicus (Norway rat)

C:Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 13-Sep-1998

C:Accession: JH0562
R: Tanabe, Y.; Masu, M.; Ishii, T.; Shigemoto, R.; Nakanishi, S.
Neuron 8, 169-179, 1992
A: Title: A family of metabotropic glutamate receptors.
A: Reference number: JH0561; MUID: 92110002
A: Accession: JH0562
A: Molecule type: mRNA
A: Residues: 1-879 <TAN>

A: Experimental source: brain
C: Comment: This protein is coupled to a G protein and evokes a variety of functions by a metabotropic glutamate receptor 4
C: Superfamily: metabotropic glutamate receptor 4
C: Keywords: G protein-coupled receptor; glycoprotein; phosphoprotein; transmembrane protein
F: 1-22/Domain: signal sequence #status predicted <SIG>
F: 23-879/Product: metabotropic glutamate receptor 3 #status predicted <MET>
F: 577-599/Domain: transmembrane #status predicted <TRI>
F: 614-634/Domain: transmembrane #status predicted <TII>
F: 646-664/Domain: transmembrane #status predicted <III>
F: 689-709/Domain: transmembrane #status predicted <TIV>
F: 735-756/Domain: transmembrane #status predicted <TV>
F: 770-791/Domain: transmembrane #status predicted <TVI>
F: 804-828/Domain: transmembrane #status predicted <VII>
F: 209,292,414,439/Binding site: carboxydrate (Asn) (covalent) #status predicted
F: 610,845/Binding site: phosphate (Ser) (covalent) #status predicted

Query Match 7.6%; Score 333; DB 2; Length 879;
Best Local Similarity 20.6%; Pred. No. 1.6e-17;
Matches 180; Conservative 132; Mismatches 313; Indels 250; Gaps 39;

Qy 36 ELHIGGFIPTAGKGGWGGQAC-----MPATRLALDDVKNQPNLLPGFKLILHS 84
Db 38 DLVLGLGLFPIKEKG--TGTEECGRINEDRGIQRLAAMLAFAIDENKYNLLPGVKLGVIH 95
Qy 85 NDS-----ECBPGLGASVYNNLYNKPQKLMLAGC-- 115
Db 96 LQTCSDTYALEQSLFEVFRASLTKVDAEYMCDPG-----SYAQENIP---LLIAGVIG 147
Qy 116 ----STVCTTVAEAKMNNLIVLCYGASSPALSDDKRPPTLFRTHPSATVHNPTRIKMLK 172
Db 148 GSYSSYSIQVANNLLRFQIQISYASTSAKLSKSDYDFARTVPPDFYQAKAMAEILRF 207
Qy 173 FGHSRVAILQQAEEVISTVEDLE-----NRCMEAGVEIVTROSFLSDPTDAVRN-LRR 225
Db 208 FNNYTVSTVASEGDYGETGTEAEFQEARLNICIT-ATAEAGVRSNIRKSDYSVIRELLQK 266
Qy 226 QDARIIVGLF-----YVVAARRVLCENYKQQLYGRAHWFFPGVYEDNMYEVLKAE 277
Db 267 PNARVV-LPMRSDDSRELIAANRV-----NASFTWV---ASDGGW-----AQE 307
Qy 278 GITCTVQOMRIAAEGHLLTTEAL-----MNQNNQNTTIS 310
Db 308 SI---VKGSEHVAYGAITTELEASHPVVRQFDYFQSLNPNYNNHNPWFDRFWEQFQCSIQ 364
Qy 311 GMTAEFRHLNQAALTEEGVDINHIDYPEGYQAPLAY--DAVWSVALAFNKTWERLTG 368
Db 365 -----NKRHHQVCDCDKHLAIDSSNYE---QESKIMFVYNAVYAMAHALMKQRTLCPN 414
Qy 369 KKLRFDF--TYTDEKETADEIYAAMNSQFL-----GVSGVFAFSQGDRIALTOI--EQMI 420
Db 415 TTKLCDAMKLLDGKKLYKEYLLKINFATPNPNKGADSIKVFDTFGDMGRYNNVFNLOOT 474
Qy 421 DGKYY--KLGY--DTQLDNLISW-----LNTEQ-----WI----- 446
Db 475 GGRYSYLKVGCHWAETSLDSDSIHWSRNSVPTSCSDPCAPNEMKNQPGDVCWCWICIPC 534
Qy 447 -----GGKVP-----QDRTIVTHLVRTVSLFLVCMC 473
Db 535 EPEYILVDEFTCMDCGPGOWPTADLSGCYNLPEDYIKWEDAWAIGPV--TIACLGFLCTC 592
Qy 474 TISSCGIFVAFALIFNWKHRR---VIOSSHPVCNTIMLFGVILICLISVILLAGIDGRF 530
Db 593 -----IVITVFIKHNTPLVKASGRELC-YILLFGVSLSYCMTF-----F 631

Qy 531 VSPPEYPKICQARAWLLSTGFTLAYGAMFSKVMRVHRETTAKTDPK--KKVEPMKLYTM 588
Db 632 FIAKPSPVICALRLGLGTSAICYSALUTKTNTARIDGKVGKGAQRPKFTSPSSQVFI 691
Qy 589 VSGLLSIDLVILLWSQIFDP--LQRYLETFFLEDVSTDDTIKIRPELEHCHESQSNMWL 646
Db 692 CLGLILQIVMVSVMWILLETPTCTRY--TLP-----EKRETVILKCNVKDSSMLI 739
Qy 647 GLVYGFGLILVFLFGLAYETRSIKVKQINDRSYVGMISYNNVVLCLITAPGVMIASQ 706
Db 740 SLTYDV--VLVILCTVYAFKTKCP-ENFNEAKFGFTMYTTCIIWLAFLPFYFTSSDY 796
Qy 707 DASFAVALAVLFCFLSMILLIFVPKVIETIRHPK 741
Db 797 RVQTTMTCISVSLSGFVVGLGLFAPKVHIVLPQPQ 831

RESULT 9

JH0561
metabotropic glutamate receptor 2 precursor - rat
C: Species: Rattus norvegicus (Norway rat)
C: Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 13-Sep-1998
C: Accession: JH0561
R: Tanabe, Y.; Masu, M.; Ishii, T.; Shigemoto, R.; Nakanishi, S.
Neuron 8, 169-179, 1992
A: Title: A family of metabotropic glutamate receptors.
A: Reference number: JH0561; MUID: 92110002
A: Accession: JH0561
A: Molecule type: mRNA
A: Residues: 1-872 <TAN>
A: Experimental source: brain
C: Comment: This protein is coupled to a G protein and evokes a variety of functions by a metabotropic glutamate receptor 4
C: Superfamily: metabotropic glutamate receptor 4
C: Keywords: G protein-coupled receptor; glycoprotein; phosphoprotein; transmembrane protein
F: 1-18/Domain: signal sequence #status predicted <SIG>
F: 19-872/Product: metabotropic glutamate receptor 2 #status predicted <MET>
F: 568-590/Domain: transmembrane #status predicted <TRI>
F: 605-635/Domain: transmembrane #status predicted <TII>
F: 637-655/Domain: transmembrane #status predicted <III>
F: 680-700/Domain: transmembrane #status predicted <TIV>
F: 726-747/Domain: transmembrane #status predicted <TV>
F: 761-782/Domain: transmembrane #status predicted <TVI>
F: 795-819/Domain: transmembrane #status predicted <VII>
F: 203,286,338,402,547/Binding site: carboxydrate (Asn) (covalent) #status predicted
F: 601,675,827,837,843/Binding site: phosphate (Ser) (covalent) #status predicted
F: 832/Binding site: phosphate (Thr) (covalent) #status predicted

Query Match 7.3%; Score 318; DB 2; Length 872;
Best Local Similarity 19.7%; Pred. No. 2.4e-16;
Matches 181; Conservative 135; Mismatches 330; Indels 274; Gaps 38;

Qy 17 LILCLIASPHLOGGVAGRP-----DELHIGGIPIAGKGGWGGQACMP----- 59
Db 4 LIGFLALLMLMGAVAEPAKVKVLTLEGDLVLGLLPVHOKGG--PAEECGPNVNEHRIQ 61
Qy 60 --ATRLALDDVKNQPNLLPGFKLILHSNDS-----EC 89
Db 62 LEAMLFALDRINRDPHLLPGVRLGAHILSDSCSDTHALEQALDFVRASLSRGADGSRHC 121
Qy 90 EPLGASVYNNLYNKPQKLMLAG--CSTVCTTVAEAKMNNLIVLCYGASSPALSDDK 147
Db 122 PDG-----SYATHSDAPTAVTGIVGYSYSDVSIQVANNLLRFQIQISYASTSAKLSK 176
Qy 148 RPTFLFRTHPSATVINPTRIKMKFGVSRVAIL-----QQAEEVFTS 190
Db 177 RYDFARTVPPDFQAKAMAEILRFNFTVSTVASEGDYGETGTEAEFAEARNICVA 236
Qy 191 TVEDLENRCMEAGVEIVTROSFLSDPTDAVRN--RRDARIIVGLFYVVAARRVLCY 248
Db 237 TSEKVGSRAMRAAFEGVVR-ALLQKPSARVAVLFTSEDAREL-----LAATQRL----- 285
Qy 249 KOOLYGRAHWVFFIGWYEDNMYEVNLKABGITCTVBEQMRIAAABGHLLTTEALM----- 300

Db 286 -----NASFTW-----ASDQWAL-----ESVAGSER-----AAGATIELASYPISDFAS 329
Qy 301 -----WNONOTTISGMTAEFR-----HRLNQAALIEEGYDINHRYPEGYQE 343
Db 330 YFQSLDPWNSRNPREFWEERHCSFRQRDCAAHSLRAVPE-----QE 375
Qy 344 APLAY--DAVNSVALAFNKTMERL-----TTGKSLRDFTYTDK----- 380
Db 376 SKIMFVNNAVYAMAHALHNHRALCPNTHLCLDAMPVNGRRILYKDFVLNVKVDAPFRPA 435
Qy 381 ETADEIYAAMNSTQFLGVSVGVAFSSQGDRIALTQIEQIMDG-----KYEKLGY----- 430
Db 436 DTDE-----VRFDFGIGYNYFTYLRAGSGRYRYOKVGTWABGLT 479
Qy 431 -DTQDNLNLSWLNTEQWIGGKVPQDR--TIVTHVLRVSLPLEVC--MC----- 473
Db 480 LDTSE--IPWASPS--AGPLPASRCSEPCIQNEKVSQ--PGEVCCWLCIPQCPYEVRLD 533
Qy 474 --TISCGI-----FVAP----- 496
Db 534 EPTCADCGIWPNASLTCFELPQBYIRWGDAAVGPVTIACLGALATLFLVLGVFVRHN 593
Qy 497 R--VIOSSHPVCNTIMLFGVILCLISVILLGIDGRFVSPPEYKICQARAWLLSTGTLA 554
Db 594 ATPVVKASGRELCYILLGVGFYCYCMTFV-----FIA-KPSTAVCTLRLRLGLGTAFSVC 646
Qy 555 YGAMFSKVRVHRFTTKAKTDPKK--VEPFKLYTWVSGLLSIDLVLISWQIFDPLQRY 612
Db 647 YSALLTKNRIARIFGGAREGAQRPFISPASQVAICLALISQILLIYAVALVVEAPGTG 706
Qy 613 LETFPLEDVSTDDIKIRPELEHESQSNMGLVYFGKGLILVFLGFLAYETRSIKV 672
Db 707 KETAPERREVTL-----RCNHRDASMLGSLAYNV--LLIALCTLYAFKTRKCP- 753
Qy 673 KOINDSRVGMISYVNVVLCITAPVGMVIAASQODASFALAVAFPCFELSMILLIFVPK 732
Db 754 ENFNEAKFIGFTMYTTCIIWLAFPIFYVTSSDYRYQTTMVCVSVLSGSLVGLCLFAPK 813
Qy 733 VLEVRHPKDKAESKYNPDS 752
Db 814 LHIILFQPKNVVSHRAPTS 833.

RESULT 10
A42916
metabotropic glutamate receptor mGluR5 - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 04-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 05-Nov-1999
C;Accession: A42916
R;Abe, T.; Sugihara, H.; Nawa, H.; Shigemoto, R.; Mizuno, N.; Nakanishi, S.
J. Biol. Chem. 267, 13361-13368, 1992
A;Title: Molecular characterization of a novel metabotropic glutamate receptor
A;Reference number: A42916; MUID:93317054
A;Accession: A42916
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-1171 <ABE>
A;Cross-references: GB:D10891; NID:g220813; PIDN:BA01711.1; PID:d1002186; PID:g220814
A;Experimental source: brain
A;Note: sequence extracted from NCBI backbone (NCBI:107749, NCBI:107750)
C;Keywords: G protein-coupled receptor; transmembrane protein

Query Match 6.9%; Score 303.5; DB 2; Length 1171;
Best Local Similarity 19.9%; Pred. No. 5.1e-15;
Matches 203; Conservative 144; Mismatches 387; Indels 287; Gaps 43;

Qy 30 VAGRPDELHIGGIFPI-----AGKGGWGGQACMPATRLALDDVKNQPNLLP 76
Db 28 VAHMPGDIIGALFSVHHQPTVDKVERKCGAVREQYGIQRVEAMLHTLERINSDPTLLP 87
Qy 77 GFKLLIHNSD-----SECEPGL-----GASVMYNLLYNPKQL 109

RESULT 11
S71376
glutamate receptor homolog - cherry salmon
C;Species: Oncorhynchus masou (cherry salmon)
C;Date: 11-Mar-1998 #sequence_revision 17-Apr-1998 #text_change 01-May-1998

Db 88 NITLGCETRSCWHSVALEBQSEIFRDSLISSEBEEGLVRCVDGSS-----SFRSKPIVG 144
Qy 110 MLLAGCSVTCTTVAEAAKWNLLIVLCYGASSPALDRKREFTLTFHPSATVHNPTRIKL 169
Db 145 VIGPSSVAIQVQNLQLFNIQIAYSATSMDLSDKTLFKFYMRVVPFSDAQARAWVDI 204
Qy 170 MKKFGWSVALIOAAEEVFISTVEDLENRCMEAGVEIVTRQSFISDPTD-----AVRNLR 224
Db 205 VKRYNWTYVSVAHTEGNYGESMEAFKDSAKEGICIAHSKYIYSNAGEQSFDKLLKKLR 264
Qy 225 RQ--DARLIIVGLFYVVAARRVLCEMYKQOLYGRAHWFEIGWYEDNW--YEV-----NL 274
Db 265 SHLPKARVAVCFEGMTVRGLLMAMRRUGLAGE-----FLILGSDGADRDDVTGQYRE 319
Qy 275 KAEGITTCVEQ-----MRTAAEGHLTTEAL--MMNQNNTTISGMTAE--EFRHR 320
Db 320 AVGGITIKLOSPDKVDFDDYILKLRPETNLRNPWFQEFQWHRFCLEGEFAQENSKYNT 379
Qy 321 LNQALIEEGYDINHRYPEGYOEAPLAY--DAVNSVALAFNKTMBRLTTGKSLRDFTYT 378
Db 380 CNSSLTLRTHV-----QDSKMGFVINALYSMAYGLHNMQMSLCPGYAGLCD--A 427
Qy 379 DKEI-ADDEIYAAMNSTQFLGVSG--VVAESSQGDRIALTQIEQIMDGKYEKLYDTOLDN 436
Db 428 MKPIDGRKLLDSLMKTNFTGVSGDMILEFENGDS-----PGRYEIMNFKEMGDY 477
Qy 437 LSWLNTQWIGGKVPQDRITV--THVLRV-SLPL----- 468
Db 478 FDYINVSQWNGELKMDDEFWSKNNIIRSVCEPCEKQIKVIRKGEVSCCWTCTPCK 537
Qy 469 -----FVC-MCTISS-----CGIF-----VAFAL 486
Db 538 ENEVFEDEYTCACQGLSGWPTDLDLTGCDLIPVQYLWGDPEPIAAVVFACGLGLATLFTV 597
Qy 487 IIFNINWKRVIQSSHPVCNTIMLFGVII-----CLISVILLGIDGRFVSPPEYKIC 540
Db 598 VIFIYRDTVPVKSRSREL--YIILAGICLGYLCTFCLIA-----KPK-- 639
Qy 541 QARAWLLSTGF--TLAYGAMFSKVRVHRFTTKAKTDPKKVPKLYTMVSGLLSID 596
Db 640 QIYCYLQIRIGLSPAMSYSAVTKNRIARILAGS-----KKICTKPRFMSACAQLVI 695
Qy 597 LVILLSWQIFDPLQRYLETFPLEDPVSTDDIKIRPELEHESQSNMGLV--YGFKG 654
Db 696 AFILICIQ---LGIIVALFIMEPPDINHYPISREVLYC---NTNLGVVTPLGNG 747
Qy 655 LILVFLGFLAYETRSIKVKQINDSRVGMISYVNVVLCITAPVGMVIAASQODASFAPA 714
Db 748 LLILSCTFYAFKTRNVA-NFNEAKYIAFTMYTTCIIWLAEVPI-----YFGSN 795
Qy 715 LAVIFCCF-----LSMLLIFVPKVIIEVIRHPKDKAESKYNPOSAL-----SKEDE 759
Db 796 YKIITMCFVSLSATVALGCMFVPKVIILAKPERNVRSAFTTSTVVRMHVGDGKSSAA 855
Qy 760 ERYOKLV-----TENEQ-----LQRL-----ITOKEEK----- 782
Db 856 SRSSLYNLNKKRCSGGETLSSNCKSVTWAQNEKSTRQHLWQRLSVHINKKNPNQTAV 915
Qy 783 IRVLRQRLVERGD---AKGTENLGATGVASAAVATTSPASLINSSAHATPAATLAIQOG 839
Db 916 IKPPPKSTENRGPCAAAGGGSGPGVAGNAGNAGCTATGGP-----EPPDAGPKALYDVAEA 970
Qy 840 E 840
Db 971 E 971

C;Accession: S71376
R;Kubokawa, K.; Miyashita, T.; Nagasawa, H.; Kubo, Y.
FEBS Lett. 392, 71-76, 1996
A;Title: Cloning and characterization of a bifunctional metabotropic receptor activated
A;Reference number: S71376; MUID:96354880
A;Accession: S71376
A;Status: not compared with conceptual translation

A: Residues: 1-1218 <KUB>
C: Keywords: glycoprotein; phosphoprotein
F: 603-625/Domain: transmembrane #status predicted <TM1>
F: 640-660/Domain: transmembrane #status predicted <TM2>
F: 672-690/Domain: transmembrane #status predicted <TM3>
F: 717-737/Domain: transmembrane #status predicted <TM4>
F: 761-782/Domain: transmembrane #status predicted <TM5>
F: 796-817/Domain: transmembrane #status predicted <TM6>
F: 828-850/Domain: transmembrane #status predicted <TM7>
F: 104_233_403_525_757/Binding site: carbohydrate (Asn) #status predicted
F: 636,699,981/Binding site: phosphate (Ser) (covalent) (by protein kinase C) #status predicted
F: 705/Binding site: phosphate (Thr) (covalent) (by protein kinase C) #status predicted
F: 892/Binding site: phosphate (Ser) (covalent) (by CAMP-dependent kinase) #status predicted

Query Match	6.9%	Score 303;	DB 2;	Length 1218;
Best Local Similarity	19.5%	Pred. No. 5.9e-15;		
Matches 173;	Conservative	144;	Mismatches 346;	Indels 222;
				Gaps 35;

[illegible]

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Db      668  YLQRLLVCLSATWCYSAIVTKYTNRIARILAGSKKKIKCTRPRPMSAWAQLVIAGLLVSVQ  727
Qy      597  LVILLSMQIFDPLQRYLETFFLEDPVSTDDIKIRPELHECHESQNSMWMLGLV--YGFKG  654
Db      728  LTLVTLILLEP-----PM-----PKVSYPISIREVFLICNTSTVGMVAPLGYNG  771
Qy      655  LILVFLGLFAYETRSIKVKQIQNSRYVGMSTYNNVVVLLCLITAPVGM-----VIASQDAS  709
Db      772  LLINACTYVAFKTRNVA-NFNEAKYIAFTWYTCIIILAFVPVIFGYSNYKIIITT----S  826
Qy      710  FAFVALAVIFCCFLSMILLIFVPKVIEWIRHPKDKAESKYNPDSAI  754
Db      827  FS-VLSLVT-----VALGCMFSPKIIYIILAKPERNVRSFTTSDVY  866

RESULT  12
JC2132
metabotropic glutamate receptor 5 A - human
C:Species: Homo sapiens (man)
C:Date: 28-Aug-1995 #sequence_revision 07-Oct-1994 #text_change 05-Jan-1999
C:Accession: JC2132
R:Nakamami, R.; Katsuki, F.; Yamamoto, T.; Nakamura, K.; Sugiyama, H.
Biochem. Biophys. Res. Commun. 199, 1136-1143, 1994
A:Title: Molecular cloning and the functional expression of two isoforms of
A:Reference number: JC2131; MUID:34197696

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RESULT 12
JC2132

metabotropic glutamate receptor 5 A - human

C:Species: Homo sapiens (man)
C:Date: 28-Aug-1995 #sequence_revision 07-Oct-1994 #text_change 05-Jan-1996
C:Accession: J02132
R:Minakami, R.; Katsuki, F.; Yamamoto, T.; Nakamura, K.; Sugiyama, H.
Biochem. Biophys. Res. Commun. 199, 1136-1143, 1994
A:Title: Molecular cloning and the functional expression of two isoforms of human met
A:Reference number: J02131: MUID:94197696

A;ACCESSION: J02132
A;Molecule type: mRNA
A;Residues: 1-1180 <MIN>

C; Residues: 1-1300; $\text{pI} = 10.7$
 C; Comment: This protein is coupled to guanine nucleotide binding proteins.
 C; Keywords: glycoprotein; neurotransmitter; receptor; transmembrane protein
 F: 580-604/Domain: transmembrane #status predicted <TM>
 F: 617-637/Domain: transmembrane #status predicted <TM>
 F: 644-664/Domain: transmembrane #status predicted <TM>
 F: 694-714/Domain: transmembrane #status predicted <TM>
 F: 738-759/Domain: transmembrane #status predicted <TM>
 F: 773-794/Domain: transmembrane #status predicted <TM>
 F: 803-827/Domain: transmembrane #status predicted <TM>

Query Match 6.9%; Score 302.5; DB 2; Length 1180;
Best Local Similarity 20.1%; Pred. No. 6.le-15;

44;

[illegible]

Db 328 EGYEVEANG-GITIKQSPEVRSFDDYFLKRLDNTNRNPFPEFWQHRFCQRLPGHLL 386

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: April 30, 2002, 10:12:08 ; Search time 9.1 seconds
(without alignments)
713.191 Million cell updates/sec

Title: US-09-715-962-2
Perfect score: 4374
Sequence: 1 MRKDWTSQVTFWFLCL.....LINSSAHATPATLAITQGE 840

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 46456 seqs, 7726236 residues

Total number of hits satisfying chosen parameters: 46456

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Pending_Patents_AA.New.*
1: /cgn2.6/pdata1/paa/PCT_NEW_COMB.pcp.*
2: /cgn2.6/pdata1/paa/US06_NEW_COMB.pcp.*
3: /cgn2.6/pdata1/paa/US07_NEW_COMB.pcp.*
4: /cgn2.6/pdata1/paa/US08_NEW_COMB.pcp.*
5: /cgn2.6/pdata1/paa/US09_NEW_COMB.pcp.*
6: /cgn2.6/pdata1/paa/US10_NEW_COMB.pcp.*
7: /cgn2.6/pdata1/paa/US60_NEW_COMB.pcp.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	359	8.2	908	1	PCT-US01-47325-3
2	358	8.2	915	1	PCT-US02-05625-67
3	355	8.1	915	1	PCT-US02-05625-8
4	355	8.1	915	1	PCT-US02-05625-71
5	354	8.1	915	1	PCT-US02-05625-69
6	350	8.0	915	1	PCT-US02-05625-73
7	222	5.1	858	6	US-10-035-045-14
8	205	4.7	839	6	US-10-035-045-21
9	190.5	4.4	852	6	US-10-035-045-4
10	180	4.1	841	6	US-10-035-045-17
11	108	2.5	403	1	PCT-US02-07826-121
12	108	2.5	403	6	US-10-097-340-121
13	104.5	2.4	911	1	PCT-US02-06415-6
14	104.5	2.4	911	1	PCT-US02-06415-8
15	103	2.4	498	5	US-09-540-209B-10405
16	103	2.4	498	5	PCT-US02-09944-663
17	102.5	2.3	728	6	US-10-036-492-5
18	100.5	2.3	253	5	US-09-540-209B-9343
19	98.5	2.3	199	5	US-09-975-553-18
20	95.5	2.2	1124	1	PCT-US02-03635-7
21	95.5	2.2	1440	5	US-09-573-655B-1303
22	94.5	2.2	716	6	US-10-036-492-11
23	94.5	2.2	762	7	US-60-370-796-25
24	94	2.1	199	5	US-09-975-553-2
25	93	2.1	262	5	US-09-540-209B-9117
26	92.5	2.1	197	5	US-09-975-553-8

ALIGNMENTS

RESULT 1
PCT-US01-47325-3
; Sequence 3, Application PC/TUS0147325
; GENERAL INFORMATION:
; APPLICANT: Genaisance Pharmaceuticals, Inc.
; APPLICANT: Bieglecki, Karyn
; APPLICANT: Chew, Anne
; APPLICANT: Choi, Julie Y.
; APPLICANT: Koshiy, Beena
; APPLICANT: Parks, Katie E.
; TITLE OF INVENTION: HAPLOTYPES OF THE GRM8 GENE
; FILE REFERENCE: GRM8_MWH-1725PCT
; CURRENT APPLICATION NUMBER: PCT/US01/47325
; CURRENT FILING DATE: 2001-11-09
; PRIOR APPLICATION NUMBER: US 60/247,576
; PRIOR FILING DATE: 2000-11-09
; NUMBER OF SEQ ID NOS: 109
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 908
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US01-47325-3

Query Match 8.2%; Score 359; DB 1; Length 908;
Best Local Similarity 21.1%; Pred. No. 1.1e-21;
Matches 204; Conservative 153; Mismatches 378; Indels 232; Gaps 44;
Qy 13 FWIFLLCLIASPHLGGVAG-RPD-ELHIGIFPIAKGGWGGQAC-----MP 59
Db 22 YWI--LTMMQTHSQEYAHRSIRVDGDIILGLFPVHARG--ERGVPCCGKKKGIHRL 77
Qy 60 ATRLALDDVNKQNLPCFKL---IL-----HNSDSECPGL 93
Db 78 AMLYAIQDKNDPDLNITGLVRILDTCSRDTYALEQSLTFVQALIEKDSADVKCANGD 137
Qy 94 GASVYMLLYNKPOKL--MLIAGCSTVCTTVAEAAKMWNLIVLCYGASSPALSQRKRPPT 151
Db 138 PP-----IFTRPKISGVICAAASSVSIMVANIILRFKIPQISYASTAPELSDNTRYDF 191
Qy 152 LFRTHPSATVHNPTRIKLMKFGWSRVAILQOAEVFTSTVEDLENROME-AGVEIVTRQ 210
Db 192 FSRVVPDPSYQAOAMVDIVTALGNVYSTLASSENGYSGVEAFQISREIGGVCIASQ 251
Qy 211 SFLSDPTDA-----VNLRRQDARIIVGLFYVVAARVLCENYKQQLYGRAHWWFFIGW 264
Db 252 KIPREPRGPEFKTIKRLETPNARAVIMFANEDDIRLEAAKKLNQSGH---FLWIG- 307


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; GENERAL INFORMATION:
; APPLICANT: Arena Pharmaceuticals, Inc.
; TITLE OF INVENTION: Endogenous And Non-Endogenous, Constitutively Activated G Protein
; TITLE OF INVENTION: Receptors
; FILE REFERENCE: AREN-0321
; CURRENT APPLICATION NUMBER: PCT/US02/05625
; CURRENT FILING DATE: 2002-02-26
; NUMBER OF SEQ ID NOS: 102
; SDFTWARE: PatentIn version 3.1
; SEQ ID NO 8
; LENGTH: 915
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US02-05625-8

      8.1%; Score 355; DB 1; Length 915;
Query Match Best Local Similarity 21.5%; Pred. No. 2.9e-21;
Matches 209; Conservative 153; Mismatches 319; Indels 292; Gaps 50;

QY 17 LCLLIA-----SPH---LQGVAGRPDELHIGGIFPIAGKGGWGQAC-----57
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 24 LLLCALAAARGQEMVAPHISIRIEGDYI-----LGLLFPVHAKG--PSGVPCGDIKREN 74

QY 58 ----MPATRLALDDVNKQPNLLPGFKL---IL-----HSNDS 87
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 75 GTHREAMLYALDQINSDPNLLPNVTILGARILDTCSRDYVALEQSLTFVQALIQKDTSDV 134

QY 88 ECEPLGLSVMYNLLYNKPKQLMLLAGC---STVCTTVAEAAKMNLLIVLCYGASSPALSD 145
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 135 RCTNGEPP-----VEVPEKVVGVIGASGVSSIMVANIILRLFIQIISYASTAPELSD 188

QY 146 RKRFPFLRTHPSATVHNPTRIKLMKFGMSRAILQOAEVEFISTVEDLENRCMEAGVE 205
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 189 DRRYDFFSRVPPDSFQAQAWDIVKALGN-----YVSTLAS-EGSYCKEGVE 236

QY 206 IVTROSLFSDPTDAVRNLR-----RQDA-----RIIVGLFYVVAARRVLC-----EMYKOOL 252
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 237 SFTQISKEAGGICIAQSVRIPOERKORTIDFDRIKQLLTDTPNSRAVVIFANDEDIKQIL 296

QY 253 YG--RA-HWFFIGIYEDNW-----YEYNLKAEGITCTVEQMRIAEG---HLTTEAL 299
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 297 AAARADQVGHFLWVGSDSWGSKINPLHOHEDAEAG-AITIQKRAATVEGFDAYFTSRTL 355

QY 300 -----MW-----NONNOTTISGMTAEF-RHRLNQAALIEGYDINHDPYEQGEAP 345
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 356 ENNRNVWFAYEENFNCKLTISGKKEDTDRKCTQERI--GKDSNYEQ--EG--KVQ 409

QY 346 LAYDAVSWVALAFNKTMERLTT-----GKKSRLDFTYTDKEIADEIYAAMNS 392
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 410 FVIDAVYAMAHALHHMNKDLCADYRGVCPMEWQAGGKKLLK-----YIRN 454

QY 393 TQFLGVSGV-VAFSSQGDRIALLTQIEQIDGKYEKLGYYDTQLDNLW-----L 440
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 455 VNFNGSAGTVPVFNKNGD-----APGRYDIFOYTNTSNPGYRLIGQWTDQL 504

QY 441 NTE--QWIGG--KVP-----L-----451
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 505 NIEDMQWKGVEIREIPASVCTLPCKPGQRKKTQKGTCCWTCEPCDGYQYQDEMTQCHP 564

QY 452 -----QDRITVT---HVLRTVSLPLFVCMCTISSCGIFVAFALIIFNWNKHR 496
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 565 YDQRPENRNTGCDIPILKLEHSPWAV-IPVFLAMLGIAT-IFVMTATIRYN-----DT 618

QY 497 RVIOSSHPCVNTIMLFGVILICLISVILLGIDGRFVSPEEPKICQARAWLLSTGFTLAYG 556
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 619 PIVRASGRELVSYLLTGIFLCYITIFLM-----IAKPD--VAVCSFRFVFLGLGMCISYA 671

QY 557 AMFSKVRVHRHTTKAK-----TDPKKKVPWKLYTMWSGLLSIDLVLILLSWOIFDPLQRYL 613
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 672 ALLTKTNIYRIFFEOGKKSVTAP-RLISPTSQLAITSLSISVQLLGLVFIWGVDPNII 730

QY 614 ETPLEDVSTDDIKIRPELEHCEGSORNSMWGLVYGFKGLIILVFLGLFLAYETRSIKVK 673

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Db 731 D-----YDBHKTMNPEQARGVLK-CDITDLQIICSL--GYSILLMVTCTVYAIKTRGVP-E 782
Qy 674 QINDSRVGMGIYNNVVVLLCLITAPVGMVIAQQDASFV-----ALAVIFCCFLSMLLI 728
Db 783 NFNEAKPIGFTMYTCIVWLAFIGI--FFGTAQSAEKLYIQTTTITISMNLSASVALGML 840
Qy 729 FVPKVIEWIRHPDKAKSKYNNPDSAISKEDSEERYOKLVTENEQLORLITQKEEKIRVLRQ 788
Db 841 YMPKVYIIIFHPELNVQKR-----KRSFKAVVTAATMSRSLSHKPSDR----- 883
Qy 789 RLVERGDAKGTTEL 801
Db 884 ---PNGEAK-TEL 892

RESULT 4
PCT-US02-05625-71
; Sequence 71, Application PC/TUS0205625
; GENERAL INFORMATION:
; APPLICANT: Arena Pharmaceuticals, Inc.
; TITLE OF INVENTION: Endogenous And Non-Endogenous, Constitutively Activated G Prot
; TITLE OF INVENTION: Receptors
; FILE REFERENCE: AREN-0321
; CURRENT APPLICATION NUMBER: PCT/US02/05625
; CURRENT FILING DATE: 2002-02-26
; NUMBER OF SEQ ID NOS: 102
; SDFTWARE: PatentIn version 3.1
; SEQ ID NO 71
; LENGTH: 915
; TYPE: PRT
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Novel Sequence
PCT-US02-05625-71

Query Match 8.1%; Score 355; DB 1; Length 915;
Best Local Similarity 21.5%; Pred. No. 2.5e-21;
Matches 209; Conservative 153; Mismatches 319; Indels 292; Gaps 50;

Qy 17 LLLCIA-----SPH---LOGGVAGRPDELHIGGIFPIAGKGGWGGQAC----- 57
Db 24 LLCLAAARACQEMVAPHISRIEGDVT-----LGLFPVHAKG--PSGVPCGDIKREN 74
Qy 58 ---MPATRLALDDVNKQPNLLPGFKL---IL-----HSNDS 87
Db 75 GIHRLEAMLYALDQINSDPNLLPNVTIGARLDTCSRDTVALEQSLTFVQALIQKTRSDV 134
Qy 88 ECEPGLGASVYNNLLYNKPQKMLLAGC--STVCTTVAEAAKMMNLLVLCYGASSPALSD 145
Db 135 RCTNGEPP-----VFVKPERVGVIGASGSSVIMVANILRLFPQIPQISYASTAPELSD 188
Qy 146 KRREPTLFRTHPSATVHNPTRIKLMKFGWGRVAILQQAEEVFISTEDLENRCMEAGVE 205
Db 189 DRRYDFRSRVPPDSFQAQAMVDIVKALGN-----YVSTLAS-EGSYGKGEVE 236
Qy 206 IVTRQSFLSDPTDAVRLR-----RODA-----RIIVGLFYVVAARRVLC-----EMYKOQL 252
Db 237 SFTQISKEAGGLCIAQSVRIPOERKDRITDPDRIIKQLLDPNPSRAVVIFANDEDIKQIL 296
Qy 253 YG--RA-HVWFFIGWYEDNW-----YEVNLKAEGITCTVEQMRIAEG---HLTTEAL 299
Db 297 AAARADQVGHFLWVSDSGWSKINPLHQHEDIAEG-AITIQPKRAVVEGDFAYFTSRTL 355
Qy 300 -----NW-----NONNOTTISGMTAEEP-RHRLNQALETGEGYDINHDPYGEQEAP 345
Db 356 ENNRNRYWFAEYWEENFENCKLTISGKKEDFDRCKTGOERI--CKDSNYEQ--EG--KVQ 409
Qy 346 LAYDAVMSVALAFNKTWERLTT-----GKSLRDTFTYDKEIADETIYAAMNS 392
Db 410 FVIDAVYAMAHLLHMMNKDLCADYRGVCPMEQAGGKLLK-----YIRN 454

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Query Match 8.1%; Score 355; DB 1; Length 915;
Best Local Similarity 21.5%; Pred. No. 2.5e-21;
Matches 209; Conservative 153; Mismatches 319; Indels 292; Gaps 50;

Qy	17	LLCLIA----	SPH-----	LOGGVAGRDELHIGIFPIACKGGWQGQC-----	57
			: :	: :	
			:	:	
Db	24	LLCALAAAAGQEAMYARISIEGDTV-----	LGLFPVHAKG--	PSGVPCGDIKREN	74
			:	:	
			:	:	
Qy	58	----MPATRIALDDVNKPQLPGFKL--IL-----	HNSDS	87	
			:	:	
			:	:	
Db	75	GIHRLERAMLVALDOINDSDPNLLPNTVLGARILDTCSRDTYALQSLSLFVQALLTKDTSDV	134		
			:	:	
			:	:	
Qy	88	ECEPGLGASVMYNLLYNKPKMLLAGC--STVCTTVAAEAKMMNLLIVLCYGASSPALSD	145		
			:	:	
			:	:	
Db	135	RCTNGPEPP-----VFVKPEKVGVIGAGSSVSIMVANILRLFQIPQISYASTAPELSD	188		
			:	:	
			:	:	
Qy	146	KRKEPTFLRTHPSATVINPTRIKLMKFGRSVAILOQAEEVFISTVEDLENRCMGAEGVE	205		
			:	:	
			:	:	
Db	189	DRRYDFFSRVVPDSFOAQAMDVIDLVKALGN-----VVSTLAS-EGSYGKGKGE	236		
			:	:	
			:	:	
Qy	206	IVTRQSFLSDPTDAVRNLr-----RQDA-----RIIVGLFTYVVAARRVLC-----EMTKQOL	252		
			:	:	
			:	:	
Db	237	SFTQISEAGSLCIAQSVRPQEKDKRTIDFDRIIKQLLDTPNSRAVVI FANDEDIKQIL	296		
			:	:	
			:	:	
Qy	253	YG--RA-HVWEFFICGW EDNW-----YFNVLKAEGITCTVEQMR TAAEG---HLITEAL	299		
			:	:	
			:	:	
Db	297	AAAKRADOVGHFLVWGSDSGSKINPLHQHEDIAEG-AITIQPKRAIVEGFDAFYFSTRLL	355		
			:	:	
			:	:	
Qy	300	-----HW-----NONNOTTISGMTAEFEF-RHRLNQALIEEGYDINHDPYEPGYOEAP	345		
			:	:	
			:	:	
Db	356	ENNRNRNVFAEYWEENFNCKLTISGSKKEDTDKCTCOERI--GKDSNYEQ---EG--KVQ	409		
			:	:	
			:	:	
Qy	346	LAYDAVMSVALAFNKMTWERITT-----GKKSLURDTFTYTDKETADEIYAAMNS	392		
			:	:	
			:	:	
Db	410	FVIDAVYAMAHALHMKNKDLCADYRGVCPEBMOAGGKKLLK-----YIRN	454		
			:	:	
			:	:	

QY 393 TOFLGSGV-VAFSSQGDRIALTOIEOMIDGKYEKLGYYDTQLDNLSW-----L 440
Db 455 VNFNGSAGTPVFNKNGD-----APGRYDIFQYQTTNTSNPGYRLIGQWTDLQ 504
QY 441 NTE--QWIGG--KVP----- 451
Db 505 NIEDMOWGKGVREIPASVCTLPCKPQORRKTQKGTCCWTCPCDGYQYQFDEMTQCHP 564
QY 452 -----QDRTIVT---HVLRTVSLPLFVCMCTISSCGIFVAFALIIFNWNKHR 496
Db 565 YDORPNENRTGCODIPIIKLEWHPWAV-IPVFLAMLGIIAT-IFVMATFIRYN-----DT 618
QY 497 RVIOSSHPCVNTIMLFGVILICLSVILLGIDGRFVSPPEYKICQARAWLLSTGTFILAYG 556
Db 619 PIVRASGRLSVLLTGIFLCYIITFLM-----IAKPD--VAVCSRRVFLGLGMCISYA 671
QY 557 AMFSKVRVHRFTTAK---TDPKKVPEWKLVTWVSGLLSIDLVILLWSQIFDPLQRYL 613
Db 672 ALLTKNRIYRIFEOGKKSVTAP-RLISPTSQAIATSSLSVQLLGVFIWFGVDPNII 730
QY 614 ETFFLEDVSTDDIKIRPELEHESQORNSMWLGLVYFKGLILVFLGLFAYETRSIKVK 673
Db 731 D----YDEHKTWNPEQARGVLK-CDITDLQIICSL--GYSILLMVTCVVAIKTRGVP-E 782
QY 674 QINDSRVGMSTYNNVVLCITAPVGMVIAQQODASFAFV-----ALAVIFCCFLSMLLI 728
Db 783 NFNEAKPIGFTMYTCIVWLAFIPI--FFGTAQSAEKLYIQTTLTISMNLSASVALGML 840
QY 729 FVPKVEIVIRHPKDAESKYNPDSAISKEDERYOKLVTENEQORLITOKEEKIRVLQ 788
Db 841 YMPKVIYIIIFHPELVQKR-----KRSFKAVVTAATMSSRLSHRPSDR----- 883
QY 789 RLVERGDAGKTEL 801
Db 884 ---PNGEAK-TEL 892

RESULT 5

PCT-US02-05625-69
; Sequence 69, Application PC/TUS0205625
; GENERAL INFORMATION:

; APPLICANT: Arena Pharmaceuticals, Inc.
; TITLE OF INVENTION: Endogenous And Non-Endogenous, Constitutively Activated G Protein
; FILE REFERENCE: AREN-0321
; CURRENT APPLICATION NUMBER: PCT/US02/05625
; CURRENT FILING DATE: 2002-02-26
; NUMBER OF SEQ ID NOS: 102
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 69
; LENGTH: 915
; TYPE: PRT
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Novel Sequence
PCT-US02-05625-69

Query Match 8.1%; Score 354; DB 1; Length 915;

Best Local Similarity 21.5%; Pred. No. 3e-21;
Matches 209; Conservative 153; Mismatches 319; Indels 292; Gaps 50;

QY 17 LCLCIA-----SPH---LOGGVAGRPDELHIGGIFPIAGKGWQGOAC----- 57
Db 24 LICALAAARGQEMYPASHIRIGEDVT-----LGLLFPVHAKG--PSGVPCGDIKREN 74
QY 58 ----MPATRALDDVKNQPNLPGFKL---IL-----HSNDS 87
Db 75 GHRLEAMLYALQDINSNPLNPNVLGARILDTCSRDTYALEBSLTFVQALLQKDTSDV 134
QY 88 ECEPGLGASWYNNLYNKKOKMLLAGC---STVCTTVAAEAKMWNILVLCYGASSPALSD 145
Db 135 RCTNGEPP-----VFVKPEKVVGVIGASGSSVIMVANILRLFOIPQISYASTAPELSD 188

RESULT 6

PCT-US02-05625-73

; Sequence 73, Application PC/TUS0205625
; GENERAL INFORMATION:

; APPLICANT: Arena Pharmaceuticals, Inc.
; TITLE OF INVENTION: Endogenous And Non-Endogenous, Constitutively Activated G Protein
; FILE REFERENCE: AREN-0321
; CURRENT APPLICATION NUMBER: PCT/US02/05625
; CURRENT FILING DATE: 2002-02-26
; NUMBER OF SEQ ID NOS: 102
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 73
; LENGTH: 915
; TYPE: PRT

QY 146 RKRPPTLFRTHPSATVNPTRIKMKKFGSRAVILQAOAEVFFSTVEDLENRCMEAGVE 205
Db 189 DRRYDEFSSRVPPDSFOQAQAMVDIVKALGN-----YVSTLAS-EGSYGERGVE 236
QY 206 IVTRQSFLSDPTDAVNLRL---RODA-----RLIVGLFYVVAARRVLC---EMYKQOL 252
Db 237 SFTQISKEAGGLCIAQSVRIPOERKORTIDFDRIIKOLLPTPNRAKRAVIFANDEIDIKOIL 296
QY 253 YG--RA-HVWFFIGWYEDNW-----YEVNLKAEGITCTVEOMRIAAEG---HLTTEAL 299
Db 297 AAKRAOVGHFLVWGSWSKINPLHOEDIAEG-AIIOPKRAIVEGDFATFRTSL 355
QY 300 -----MW-----NONNOTTISGMTAEF-RHRLNOALIEEGYDINHDPGYPEAP 345
Db 356 ENNRNRYFAEYWEENENCKLTISGSKKEDTRKCTQGERI--GKDSNYEQ--EG--KVQ 409
QY 346 LAYDAVMSVALAFNKTWERLTT-----GKSLRDFTYTDEKIDEIADYAAWNS 392
Db 410 FVIDAVYAMAHALHMMKNDLCADYRGVCPMEQAGKKLLK-----YIRN 454
QY 393 TOFLGSGV-VAFSSQGDRIALTOIEOMIDGKYEKLGYYDTQLDNLSW-----L 440
Db 455 VNFNGSAGTPVFNKNGD-----APGRYDIFQYQTTNTSNPGYRLIGQWTDLQ 504
QY 441 NTE--QWIGG--KVP----- 451
Db 505 NIEDMOWGKGVREIPASVCTLPCKPQORRKTQKGTCCWTCPCDGYQYQFDEMTQCHP 564
QY 452 -----QDRTIVT---HVLRTVSLPLFVCMCTISSCGIFVAFALIIFNWNKHR 496
Db 565 YDORPNENRTGCODIPIIKLEWHPWAV-IPVFLAMLGIIAT-IFVMATFIRYN-----DT 618
QY 497 RVIOSSHPCVNTIMLFGVILICLSVILLGIDGRFVSPPEYKICQARAWLLSTGTFILAYG 556
Db 619 PIVRASGRLSVLLTGIFLCYIITFLM-----IAKPD--VAVCSRRVFLGLGMCISYA 671
QY 557 AMFSKVRVHRFTTAK---TDPKKVPEWKLVTWVSGLLSIDLVILLWSQIFDPLQRYL 613
Db 672 ALLTKNRIYRIFEOGKKSVTAP-RLISPTSQAIATSSLSVQLLGVFIWFGVDPNII 730
QY 614 ETFFLEDVSTDDIKIRPELEHESQORNSMWLGLVYFKGLILVFLGLFAYETRSIKVK 673
Db 731 D----YDEHKTWNPEQARGVLK-CDITDLQIICSL--GYSILLMVTCVVAIKTRGVP-E 782
QY 674 QINDSRVGMSTYNNVVLCITAPVGMVIAQQODASFAFV-----ALAVIFCCFLSMLLI 728
Db 783 NFNEAKPIGFTMYTCIVWLAFIPI--FFGTAQSAEKLYIQTTLTISMNLSASVALGML 840
QY 729 FVPKVEIVIRHPKDAESKYNPDSAISKEDERYOKLVTENEQORLITOKEEKIRVLQ 788
Db 841 YMPKVIYIIIFHPELVQKR-----KRSFKAVVTAATMSSRLSHRPSDR----- 883
QY 789 RLVERGDAGKTEL 801
Db 884 ---PNGEAK-TEL 892

QY	17	LLCLIA-----SPH---LQGVAGRDELHIGFIPTAGKGGWGGQAC-----	57
DB	24	LICLAAAAAQEMAPHSTRIEGDVT-----LGLFPVHAKG--PSGYPCGDIKREN	74
QY	58	-----MPATRALDDVNKQPNLLPGFKL--TL-----HSNDS	87
DB	75	GIHRLAEMLYALDOINDSPNLLPNVTLGARILDTCSRDTYALEOSLTFVQALIOKDTSDV	134
QY	88	ECEPGLGASVMYNLLYNKPQKMLLAGC--STVCTTVAEAAKMNNLIVLCYGASSPALSD	145
DB	135	RCTNGEPP-----VFVKPEKVVIGASGSSVIMVANILRLFOIPQISVASTAPELSD	188
QY	146	RKRPPTLFRHPSATVINPTRIKLKKFGKRSRVALLOQAEVEFISTVEDLENRCMEAGVE	205
DB	189	DRRYDFESRVVPPDSFOQAQAMVDIVKALGN-----YVSTLAS-BGSGYGEKGV	236
QY	206	IVTROSLSDPTDAVRNLR-----RQDA-----RIIVGLFYVVAARRVLC-----EMVKOOL	252
DB	237	SFTQISKEAGLCTAQSVRPOEKRDTIDFDRIIKQLLDTPNRAVVIFANEDIKQIL	296
QY	253	YG--RA-HVMFFIGWYEDNW-----YEVNLKAEGITCTVEQMRIAABG---HLTTEAL	299
DB	297	AAAKRADQVGHFLVWGSDSWGSKINPLHQHEDIAEG-AITIQPKRATVEGFDAYFTSRTL	355
QY	300	-----MW-----NONNQTTISGMTAEFP-RHRLNQALIEEGYDINHDPYPEGYQAP	345
DB	356	ENNRNRYWFAEYWEENFNCKLTISGSKEDDRCTQGERI--GKDSNYEQ--EG--KVQ	409
QY	346	LAYDAVSWALAFNKTWERLTT-----GKSLRDFTYTDKEIADEIYAAMNS	392
DB	410	FVIDAVYAMAHLMHMKDKADYRGVCPMEQAGGKKLK-----YIRN	454
QY	393	TQFLGVSGV-VAFSSOGDRIALTQIEQMIDGKYBKLGYDYDFOLDNLW-----L	440
DB	455	VNFGSAGTPVMFNKNGD-----APGRYDIFQYQTTNTSPGYRLIGQWTDQLQL	504
QY	441	NTE--QWIGG--KVP-----	451
DB	505	NIEDMQMGKGVREIPASVTLPCCKPGORKTKQTPCCWTCPCDGYQYQFDEMTQCQHP	564
QY	452	-----QDRTLVT---HVLRTVSLPLFCVCMCTISSCGIFVAFALIFINWKNHR	496
DB	565	YDQRPENRTGCQDIPILIKLEHSPWAV-IPVFLAMLGITAT-IPVWATFRYN-----DT	618
QY	497	RVIQSSHPVCNTIMLFGVIITCLISVILLGIDGREVSPPEYPKICQARAWLLSTGFTLAYG	556
DB	619	PIVRASGRELSYLLTGIFLCYIITFLM-----IAKPD--VAVCSFRVRFLGLMCISYA	671
QY	557	AMFSKVVVRVHRTTKAK---TDPKKVPEPKLYTWMVGLSLSIDLVILLSQWIFDPLQRYL	613
DB	672	ALLTKNRIYRIFBQGGKSVTAP-RLISPTSQLAITSSLSVQLLGVFIWFGVDPNNIUI	730
QY	614	ETPPLDPVSTDDIKIRPELEHCHESQORNMSWGLVVGFKGLIILVFLFLAYERSTIKVK	673
DB	731	D-----YDEHTMNPQARGVLK-CDITDLQICSL--GYSILLMVTCTVYAKTRGPV-E	782
QY	674	QINDSRYVGMISVNVVLCILITAPVGMVIAQQDASFAFV-----ALAVIFCCFLSMLLI	728
DB	783	NFNEAKPKGFTMYTTCIVLWAFIPi--FFGTAQSAEKLYIQTTLTISMNLSASVALGML	840
QY	729	FVPKVIIEIRHPDKAKSKYNPDSAISKEDERYOKLIVTENEQLORLITQKEEKIRVLQ	788
DB	841	YMPKVYIIIEHPELNVOKR-----KRSPKAVYATATMSRSLSHKPSDR-----	883

Db 511 GQVRRVKGFGSCCYDCVCKAGSYRKHDPDFTCTPCGKQDQWSEKSTTCLPRRPKFLAWG 570
Qy 460 VLRVSLPLFVCM---CTISSCGIFVAFALIIFNINMKHRRVIOSSHPVONTIMLFGVII 516
Db 571 EPVAVLSLLLLCLVLGLTLAALGLFVHY-----NDS--PLVQASG---GSLFCFG-LI 617
Qy 517 CL-----ISVILGIDGRFVSPPEYKICQARAWLLSTGFTLAYGAMPSKVRVHRFTTKA 572
Db 618 CLGLFCLSVLLFPGRPRSAS-----CLAQOPMAHLPLRGCLSTLFLQAAEIP----- 664
Qy 573 KTDPKKKVE-----PWKLYTMVSGLLSDIIVLLSMQIFDPLQRYLET 615
Db 665 -----VESEPLSWANWLCVLRGPMAWLVL--LATLVEAALCAW-----YLMA 707
Qy 616 FLEDPVSTDDIKRPE--LEHCEQSNMGLGLVYGRKLIILVFLGFLAYETRISKVK 673
Db 708 FPPE-----VVTDMQVLPTEVLEHCR-MRSWVSLGLVH-IINAVLAFCLFLGTFLVQSQPG 761
Qy 674 QINDSYVGMISYNNVVCLITAPGVGMVIAQQDASFAFVALAVIFCCFLSMLLIIF-VPK 732
Db 762 RYNRARGLAFAMLAYFIWVSFVP--LLANQVAVQPAVQMGAAILFCALGILATPHLPK 818
Qy 733 VIEVI-----RHPKDKAESKYNPDSAISKEDE 759
Db 819 CYVLLMWLPENLTQEFFLGRSPKEASDNGSGSEATRHS 858

RESULT 8

US-10-035-045-21

; Sequence 21, Application US/10035045

; GENERAL INFORMATION:

; APPLICANT: ADLER, JON ELLIOT

; APPLICANT: LI, XIAODONG

; APPLICANT: STASZEWSKI, LENA

; APPLICANT: O'CONNELL, SHAWN

; APPLICANT: ZOZULYA, SERGEY

; TITLE OF INVENTION: TIR TASTE RECEPTORS AND GENES ENCODING SAME

; FILE REFERENCE: 078003-0280681

; CURRENT APPLICATION NUMBER: US/10/035,045

; CURRENT FILING DATE: 2002-01-03

; PRIOR APPLICATION NUMBER: 60/259,227

; PRIOR FILING DATE: 2001-01-03

; PRIOR APPLICATION NUMBER: 60/284,547

; PRIOR FILING DATE: 2001-04-19

; NUMBER OF SEQ ID NOS: 24

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 21

; LENGTH: 839

; TYPE: PRT

; ORGANISM: Homo sapiens

US-10-035-045-21

Query Match 4.7%; Score 205; DB 6; Length 839;
Best Local Similarity 19.4%; Pred. No. 5e-09;
Matches 174; Conservative 144; Mismatches 335; Indels 244; Gaps 43;

Qy 16 FLICLIASPHLOGVAGRPDELHIGGFITAGKGGWOG-----GQ 55
Db 13 FLWVIAEP-AENSDFYLPDGYLLGLLSL--HANMKGIHLNPLQVPMCKEYEVKVIY 69
Qy 56 ACPATRLADDVKNQPNLPGFKLILHSD-----SECPGLGASVWY-----NLL-- 102
Db 70 NLQAMRFAVEEINNDSLLPGVLLGYEIVDVYISNNVQ-----VLYFLAHEDNLLPI 124
Qy 103 -----YINKPKMLLAG--CSTVCTTVAEAAKMNLIIVLCYCASSPALSDRRKRPFLRTH 156
Db 125 QEDYSNYSRVAVIGPDNSESVMVANFSLFLPQITYSAISDELDRKVRFPALLRTT 184
Qy 157 PSATVHNPTRIKLMKFGSRVAILQAE-----EVPFSTVE 193
Db 185 PSADHHVEAMVOLMLHFRWNIIIVLVSSDTYGRDNGOLLGERVARRDICIATFQETLPTLQ 244

Query Match

4.4%; Score 190.5; DB 6; Length 852;

Qy 194 DLENRCMEAGVEIIVTROSFSDPTDAVRNLRQDARIIVGLFVYVVAARRVCEMYKQOLY 253
Db 245 PNQWNTSEERORLVT-----IVDKLQOSTARVVVVVSPDLTYLHYFFNEVLQRNFT 294
Qy 254 GRAHVWFFI-CWYED---NMVEYNLKAEGITCTVEQMRIAAGHLTTEALMNQN--- 304
Db 295 GA--VWIASESAIDPVLHNITELGHTGFTGITIQSVPIG---FSEFHWGQAGPP 348
Qy 305 --NOTTISGMTAEFRHLNQAALIEGYDINHRYPEGYQEAFLAYDAVMSVALAFNKT 362
Db 349 PLSTSQSYTCQECNCLNATL-----SFNTILRLSGERVVSYVSAVAVAHLSLL 403
Qy 363 --ERLTGKSLRDTFTYDKIEADIYAAAMNSTOFLGVGVVAFSSQGDRIALTQIEMI 420
Db 404 GCDKSTCTKRVVYEW---QLLEBIW---KVNFTLHDHQIFFDPQGD-VALLH--EIV 451
Qy 421 DGKYEK-----LGYDDTQ-----LDNLSWLNTEQMI-----GGK----- 449
Db 452 QMWDRSQNPQSVASYYPQLQRQKNIQDISHNTVNNTPHSMCSKRCQSGOKKPKVGIH 511
Qy 450 -----VP-----QDRT-----IVTHVLRVTSVPL 468
Db 512 VCCPECIDCLPGLNHTEDYEEOACPNNEWSQSETSCPKRQLVFLNHEAPTIAVAL 571
Qy 469 FVCMCTISSCGIFVAFALIIFNINMKHRRVI--QSSHPCVNTIMLFGVILCLISVILLGI 526
Db 572 LAALGFLSTAILVIF-----WRHFQTPIVRSAGGPMC-FLML---TLLLVAVWVVPV 620
Qy 527 DGRFVSPPEYPKI--CQARAWLLSTGFTLAYGAMPSKVRVHRFTTKAKTDPKK---VE 581
Db 621 ---YVGP---BKVSTCLCRQALFPLCFTICISIAVRSFQIVCAFKMASRFRAYSYVVR 674
Qy 582 PWKLYTMVSGLLSDIIVLLSMQIFDPLQRYLETPELDPVSTDDIKRPELEHCE-SQ 640
Db 675 YQGPVSMFAFITVLKMWIVVIGMLATGLSPTRTD-----DDPKI--TIVSCNPNY 724
Qy 641 RNSMLGLVYGFGLVGLFLAYETRISIKVKQINDSYVGMST-----YNNVVLCLITA 696
Db 725 RNSLLFNTSLDL--LLSVVGFSAFYMGKELPT-NYNEAKFTLSMTFTVTSVSLCTFMS 781
Qy 697 PVGMVIAQQDASFAFVALAVIFCCFLSMLLI-----FVPKVEIVIRHPKDKAESKYN 749
Db 782 AYSGLV-----VTIVDLVTVLNLALSLGYPGPKCYMILFYPERNTPAYFN 828

RESULT 9

US-10-035-045-4

; Sequence 4, Application US/10035045

; GENERAL INFORMATION:

; APPLICANT: ADLER, JON ELLIOT

; APPLICANT: LI, XIAODONG

; APPLICANT: STASZEWSKI, LENA

; APPLICANT: O'CONNELL, SHAWN

; APPLICANT: ZOZULYA, SERGEY

; TITLE OF INVENTION: TIR TASTE RECEPTORS AND GENES ENCODING SAME

; FILE REFERENCE: 078003-0280681

; CURRENT APPLICATION NUMBER: US/10/035,045

; CURRENT FILING DATE: 2002-01-03

; PRIOR APPLICATION NUMBER: 60/259,227

; PRIOR FILING DATE: 2001-01-03

; PRIOR APPLICATION NUMBER: 60/284,547

; PRIOR FILING DATE: 2001-04-19

; NUMBER OF SEQ ID NOS: 24

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 4

; LENGTH: 852

; TYPE: PRT

; ORGANISM: Homo sapiens

US-10-035-045-4

Best Local Similarity		18.9%;	Pred. No. 8e-08;	
Matches		173;	Conservative	144;
		Mismatches	309;	Indels
		291;	Gaps	43;
Qy	11	VTFWIFL-----LCLTASPHLOGVAGRPDELIHGIGFPI--AKGGWQ-----	52	
Db	9	LSLWALLHPGTCAPCLCSOQLRMKG-----DYVLGGLFPLGEEAEAGLRSRTSPSPV	61	
Qy	53	-----GQOACMPATRLADDVNKOPNLLPGFKLILHNSDSECP--GLGASVMY-----	99	
Db	62	CTRFSSNGLLWALAMKMAVEEINNKSOLLPLGLRLGYDLFTCEPVMAMKPSLMFLAKAG	121	
Qy	100	-----NLLYNPKMLLAGCSTVCTTVAEAAKWNLLVL---CYGASSPALSDRKR	148	
Db	122	SRDIAAYNYTQYQPRVLAVLGPSSSELAMV--TGKFFSFFLMPOVSYSGAMELLSARET	179	
Qy	149	FPTLFRTHPSATVNPTRIKLMKKFGRSVAILOQAAEV-----FISTVEDELENRCM-E	201	
Db	180	FPSFRTVPSPDRVLATAAEILLOEGWNWVAALGSDDEYGRGLSIFALAAARGICIAH	239	
Qy	202	AGVEIVTR--OSFISDPTDPAVRNLRRODARIIVGLFYVVAARRVLCEMYKOOLYGRAHVW	259	
Db	240	EGLVPLPRADDSRLGKVQDVLHOVNOSQVVV-LFASVHA-----AHAL	283	
Qy	260	FFIGHYEDNWEVNLKABGICTVEOMRIAREGHILTTEAM-----	300	
Db	284	FN-----YSISRLS-----PKWVASEAMLTSLVMGLPGMAOMGTVLGFLORGA	329	
Qy	301	----WNQNOTTISGMTAEERHRLNOALIEBGY--DINHDRYPE-----GY	341	
Db	330	QLHFEPPQVVKTHALATDAPFCSALGER--EOGLEEDYVGORCPDCCITLQNVSAGLNH	387	
Qy	342	QEAPLAYDAVMSVALAFNKTKMERLTG-----KKSRLDFTY-----	377	
Db	388	HOTESVAAVYSAQALHNTLOCNASGCPADDPKVPWOLLENMNYNLTHVGLGLPLRFDSS	447	
Qy	378	--TKEIADEIYAAAMSTQFLGVSGVVAFFSOGDRIALTO-----IEQMIDGK	423	
Db	448	GNVDMEYDLKLMWQGSVPRLHDVGRFNGSLRTERLKIWHITSQKQPVSRCSRQCQEGQ	507	
Qy	424	YEKL-----GYDITOLDNL--SWLNTQEWIGKVPQDRT-----	455	
Db	508	VRVKGFHSFCYDCVDCBAGSTRQNPDDIACTFCGODEM-----SPERSTRFRRSREFLA	563	
Qy	456	----IVTHVLRTVSLPLFCVMCTTSSCGIFVAFALIIFENIWNKHRR-----VIQSSHPVCNT	508	
Db	564	WCEPAVLLLLLLLSIALGL--VLAALGLFV-----HHRDSPLVQASG---GP	605	
Qy	509	IMLGEVI---ICLISVILLGIDGRFVSPEYBPKICQARAWLLSTGFTFLYAMGSKVWR	564	
Db	606	LACFGLVCLGLVCLSVLLFPG-----QPSPARCLAQOPLSHLPLTGCLSTLFLQAAE	657	
Qy	565	VHRTTRAKTDPKKVE-----PWKLYTWVSGLLSIDLVILLWSQIFD	607	
Db	658	IF-----VESEPLSNADRLSGCLRGPFAMWLVVLLAMLV--EVALCTW-----	698	
Qy	608	PLQRYLTFPLEDPVSTDDTKIRPE--LEHCESORNSMWL--GLVYGFKGILILVFGFLA	664	
Db	699	----YLVAFP--PEVYTDWHMLPTEALVHC---RTRSVSFEGLAHA--TNATLAFCLFGL	747	
Qy	665	YETRISKYQINDSRVYGMVINYVVLCLITAPYGMVITASOODASFAFVALAIFCCFLS	724	
Db	748	TFLVRSOPGCYNRRAGLTFAMLAYFITWVSFVP--LLANOVVLLRPVAVQMGCALLLCVLG	804	
Qy	725	MLLIF-VPKVIETVIRHP	740	
Db	805	ILAAFHLPRCYLLMRQP	821	

RESULT 10
US-10-035-045-17
; Sequence 17, Application US/10035045
; GENERAL INFORMATION:
; APPLICANT: ADLER, JON ELLIOT

? APPLICANT: LI, XIAODONG
 ? APPLICANT: STASZEWSKI, LENA
 ? APPLICANT: O'CONNELL, SHAWN
 ? APPLICANT: ZOZULYA, SERGEY
 ? TITLE OF INVENTION: T1R TASTE RECEPTORS AND GENES ENCODING SAME
 ? FILE REFERENCE: 078003-0280681
 ? CURRENT APPLICATION NUMBER: US/10/035.045
 ? CURRENT FILING DATE: 2002-01-03
 ? PRIOR APPLICATION NUMBER: 60/259,227
 ? PRIOR FILING DATE: 2001-01-03
 ? PRIOR APPLICATION NUMBER: 60/284,547
 ? PRIOR FILING DATE: 2001-04-19
 ? NUMBER OF SEQ ID NOS: 24
 ? SOFTWARE: PatentIn Ver. 2.1
 ? SEQ ID NO 17
 ? LENGTH: 841
 ? TYPE: PRT
 ? ORGANISM: Homo sapiens
 ? US-10-035-045-17

Query Match 4.1%; Score 180; DB 6; Length 841;
Best Local Similarity 17.8%; Pred. No. 5.7e-07;
Matches 162; Conservative 134; Mismatches 287; Indels 326; Gaps 41;

[illegible]

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QY 575 DPKKVPEPW-----KLYTWVSGLLSIDLVILLSW-QIFDPL-----QRYLETFPLEDPV 622
Db 669 -----FYHAWVNGHAGLFVNMIS--AAQLICLTWLVVWTPLPAREYQRPPLHVMLE--- 719
QY 623 STTDDIKIRPELEHESQSRNMLGLVYGFKGLILVFLGLAYETRSIKVKQINDSRVVG 682
Db 720 -----C-TETSLGFIPLAFLYNGLLSISAFACSYLGKDLPE-ENYNEAKCVT 763
QY 683 MS-IYNV--VLCITA-----PVGMIASQODASFAFVALAVIFCCFLSMLLIFVP 731
Db 764 FSLLFNFVSWIAFTTASVDYGRKYLPAANMAGLSLSSGFG-----YFLP 810
QY 732 KVIEVIRHP 740
Db 811 KCVILCRP 819
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RESULT 11
PCT-US02-07826-121
; Sequence 121, Application PC/TUS0207826
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc. et al.
; TITLE OF INVENTION: Nucleic Acid Molecules and Proteins For The Identification,
; FILE REFERENCE: MRI-030PC
; CURRENT APPLICATION NUMBER: PCT/US02/07826
; PRIOR FILING DATE: 2002-03-14
; PRIOR APPLICATION NUMBER: 60/276,025
; PRIOR FILING DATE: 2001-03-14
; PRIOR APPLICATION NUMBER: 60/325,149
; PRIOR FILING DATE: 2001-09-27
; PRIOR APPLICATION NUMBER: 60/276,026
; PRIOR FILING DATE: 2001-03-14
; PRIOR APPLICATION NUMBER: 60/324,967
; PRIOR FILING DATE: 2001/09/26
; PRIOR APPLICATION NUMBER: 60/311,732
; PRIOR FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: 60/325,102
; PRIOR FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: 60/323,580
; PRIOR FILING DATE: 2001-09-19
; NUMBER OF SEQ ID NOS: 363
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 121
; TYPE: PRT
; LENGTH: 403
; ORGANISM: Homo sapiens
PCT-US02-07826-121
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Query Match 2.5%; Score 108; DB 1; Length 403;
Best Local Similarity 19.5%; Pred. No. 0.16;
Matches 50; Conservative 39; Mismatches 97; Indels 70; Gaps 9;

QY 466 LPLFVCMC-----TISCGIFVAFALIIF-----NIWNKRRVIOSSH--PVC 506
Db 42 LPQVSLCDLDAIWGIIVVEAVAGALITLLMLLILVRLPFKEKEKSPVGLHFLFL 101
QY 507 NTIMLFGVILCLISVILLGIDGRFVSPEEYPKICQARAWLLSTGFTLAYGAMFSKVRVH 566
Db 102 GTLGLFGLTFAFI-----QDEETICSVRRFLWGLVLCFCSCLLSQAMRVR 148
QY 567 RFTTKARTDPKKVPEKWKLYTMVSGLLSIDLVILLSQIFDPLQRYLETFFLEDVSTTD 626
Db 149 RL-VRHGTGP-----AGQVLGALCLMLVQVITAVEHLVTLVR--DTRPA----- 192
QY 627 DIKIRPELEHESQSRNMLGLVYGFKGLILVFLGLAYETRSIKVKQINDSRVVGSIY 686
Db 193 -----CAYEPMDFVMALIYDMVLLVVTGLGLAFTLTCGKFKRWKLNKA----- 234
QY 687 NVVVLCLITAPGVMI 702
Db 235 -----FLLITAFLSVLI 246
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RESULT 12
US-10-097-340-121
; Sequence 121, Application US/10097340
; GENERAL INFORMATION:
; APPLICANT: John MDNAHAN
; APPLICANT: Manjula GANNAVAPARU
; APPLICANT: Sebastian HOERSCH
; APPLICANT: Shubhangi KAMATKAR
; APPLICANT: Steve G. KOVATS
; APPLICANT: Rachel E. MEYERS
; APPLICANT: Michael MDRISEY
; APPLICANT: Peter DLANDT
; APPLICANT: Ami SEN
; APPLICANT: Peter VEIBY
; APPLICANT: Gordon B. MILLS
; APPLICANT: Robert C. BAST, Jr.
; APPLICANT: Karen LU
; APPLICANT: Rosemarie SCHMANDT
; APPLICANT: Xumei ZHAO
; APPLICANT: Karen GLATT
; TITLE OF INVENTION: Nucleic Acid Molecules and Proteins For The Identification,
; FILE REFERENCE: MRI-030
; CURRENT APPLICATION NUMBER: US/10/097,340
; CURRENT FILING DATE: 2002-03-14
; PRIOR APPLICATION NUMBER: 60/276,025
; PRIOR FILING DATE: 2001-03-14
; PRIOR APPLICATION NUMBER: 60/325,149
; PRIOR FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: 60/276,026
; PRIOR FILING DATE: 2001-03-14
; PRIOR APPLICATION NUMBER: 60/324,967
; PRIOR FILING DATE: 2001/09/26
; PRIOR APPLICATION NUMBER: 60/311,732
; PRIOR FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: 60/325,102
; PRIOR FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: 60/323,580
; PRIOR FILING DATE: 2001-09-19
; NUMBER OF SEQ ID NOS: 363
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 121
; TYPE: PRT
; LENGTH: 403
; ORGANISM: Homo sapiens
US-10-097-340-121
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Query Match 2.5%; Score 108; DB 6; Length 403;
Best Local Similarity 19.5%; Pred. No. 0.16;
Matches 50; Conservative 39; Mismatches 97; Indels 70; Gaps 9;

QY 466 LPLFVCMC-----TISCGIFVAFALIIF-----NIWNKRRVIOSSH--PVC 506
Db 42 LPQVSLCDLDAIWGIIVVEAVAGALITLLMLLILVRLPFKEKEKSPVGLHFLFL 101
QY 507 NTIMLFGVILCLISVILLGIDGRFVSPEEYPKICQARAWLLSTGFTLAYGAMFSKVRVH 566
Db 102 GTLGLFGLTFAFI-----QDEETICSVRRFLWGLVLCFCSCLLSQAMRVR 148
QY 567 RFTTKARTDPKKVPEKWKLYTMVSGLLSIDLVILLSQIFDPLQRYLETFFLEDVSTTD 626
Db 149 RL-VRHGTGP-----AGQVLGALCLMLVQVITAVEHLVTLVR--DTRPA----- 192
QY 627 DIKIRPELEHESQSRNMLGLVYGFKGLILVFLGLAYETRSIKVKQINDSRVVGSIY 686
Db 193 -----CAYEPMDFVMALIYDMVLLVVTGLGLAFTLTCGKFKRWKLNKA----- 234
QY 687 NVVVLCLITAPGVMI 702
Db 235 -----FLLITAFLSVLI 246
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Query Match	2.4%	Score 104.5;	DB 1;	Length 911;
Best Local Similarity	20.2%	Pred. No. 1.1;		

Qy	215	DPTDAVRLRRQDARIIVGLFVVVAARVLCEMYKQOLYGRA-----HVVFFIGW 264 : : : : : : :
Db	198	NPID-MDSLTFREQOKTVDFLYNAGRKEILS---NPQRYGKVTRPVDRENVKRCVGL 253 : : : : : : :
Qy	265	YEDNWYEVLNKAEGITCTVFQMRLAAEGHLTTALMWNQNQTITSGMTAEERH----R 320 : : : : : : :
Db	254	PGDTLQIIN-----GOVMIDGRAKENPENLQFNFYVQTGPYTTEEMFRELGISK 303 : : : : : : :
Qy	321	LNOALLIEGYDINHDPYEGVOEAPL-----AYDAVWSVALAFNKTWERLTITGKKSLR 373 : : : : : : :
Db	304	AQRUTPEGAS-----YEEGLIELGLDGRNAOQGLNPVYHLPIT-KMYDTLSGNKKLVG 357 : : : : : : :
Qy	374	DFTYTDREIADEIYAA--MNSTQFLGVSGVAVFSQQGDRIALT-----Q 415 : : : : : : :
Db	358	KVIEPEYSGEVYPPLNTHHNRSYGPIWIPAKGATITLTPDLNLPIERCITYAEGNK 417 : : : : : : :
Qy	416	IEQMIDGKY---EKLGYDYDTOLDNLSQL-----NTEQWTGGKVPQDRTIVTHVLRT 463 : : : : : : :
Db	418	LEQKEDGIYINGVKTNQYTFEQMD-YYWMGMGNRHNSADSRYW--GFVPEDHVVGKPIVWW 474 : : : : : : :
Qy	464	VSL 466 : : : : : : :
Db	475	LSL 477 : : : : : : :

```

198 NPID-MDSLTREQQKTVIYDIYNAGRKEILS---NPQRYGKVVTPRDRENNVVRCVGL 253
265 YEDNMWYEVNLKAEGITCTVEQMRLAAEGHLLTTEALMWNQNONOTTISGWTAEFRH----R 320
254 PGDTLIQIIN-----GQVMIDGKALENPENLQFNFYVQTTGPITYTEEMFRELGISK 303
321 LQOALLBEGYDINHDPYPEGYQEAFL-----AYDAVMSVALAFNKMTERRLTTCCKSLR 373
304 ADQRLTPGEGAS-----YBEGLIELGDGNAOGGLNPVYHLPLT-KKWYDTLSGNKKLVG 357
374 DFTYTDKEIADIYAA-MNSTQFLGSGVWAFSSGDRIALT-----Q 415
358 KIVIEPEEYSEGVYPLNLNTHWNRSYDGPWIWPAKGATITLTPDLNPIYERCITAYEGNK 417
416 IEQMIDGXY---EKLGYDYDTOLDNLSWL-----NTEOWIGKGVPQDRITVTHVLRT 463
418 LEQKEDGIYINGVKTNQYTFQMD-YVWMGDNRHNSADSRYW--GFVEDHVVGVGPVWV 474
464 VSL 466
475 LSL 477

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Search completed: April 30, 2002, 10:15:50
Job time: 222 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: April 30, 2002, 10:10:58 ; Search time 27.28 Seconds
(without alignments)
2280.849 Million cell updates/sec

Title: US-09-715-962-2
Perfect score: 4374
Sequence: 1 MRKDMTSDGAVTFWFLCL.....LINSSAHATPAATLAIQTQE 840

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 522463 seqs, 74073290 residues

Total number of hits satisfying chosen parameters: 522463

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

- Database : A_Geneseq_1101.*
- 1: /SIDSB/gcgdata/geneseq/geneseq/AA1980.DAT.*
 - 2: /SIDSB/gcgdata/geneseq/geneseq/AA1981.DAT.*
 - 3: /SIDSB/gcgdata/geneseq/geneseq/AA1982.DAT.*
 - 4: /SIDSB/gcgdata/geneseq/geneseq/AA1983.DAT.*
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 - 8: /SIDSB/gcgdata/geneseq/geneseq/AA1987.DAT.*
 - 9: /SIDSB/gcgdata/geneseq/geneseq/AA1988.DAT.*
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 - 19: /SIDSB/gcgdata/geneseq/geneseq/AA1998.DAT.*
 - 20: /SIDSB/gcgdata/geneseq/geneseq/AA1999.DAT.*
 - 21: /SIDSB/gcgdata/geneseq/geneseq/AA2000.DAT.*
 - 22: /SIDSB/gcgdata/geneseq/geneseq/AA2001.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	4374	100.0	840	22	AAB86159 D. melanogaster GA
2	2035	46.5	844	19	AAW40119 Human GABA-BR1b re
3	2035	46.5	844	20	AAW28839 Human GABABR1b rec
4	2035	46.5	844	20	AAW14102 Human G-protein co
5	2035	46.5	844	21	AAW32467 Human GABAB recept
6	2034.5	46.5	899	20	AAW14107 Rat GABA-BR1b rece
7	2032	46.5	844	19	AAW40118 Canine GABAB recep
8	2031.5	46.4	964	20	AAW14105 Human GABABIAA rec
9	2030.5	46.4	960	21	AAW83145 Human GABABR1a rec
10	2030.5	46.4	961	20	AAW28838 Human gamma-amino-
11	2030.5	46.4	961	20	AAW29798

12	2030.5	46.4	961	20	AAW14101 Human GABAB recept
13	2030.5	46.4	1323	20	AAW49133 GABA-BR1a*Gqo5 fusi
14	2029.5	46.4	793	19	AAW40117 Human GABA-BR1a/B
15	2029.5	46.4	892	20	AAW14109 Human GABAB recept
16	2029.5	46.4	960	19	AAW40116 Rat GABA-BR1a rece
17	2029	46.4	962	22	AAB50090 Murine GABA-B-R1a.
18	2028.5	46.4	960	20	AAW29797 Murine gamma-amino
19	2026	46.3	844	20	AAW28842 Rat GABABR1b recep
20	2026	46.3	844	20	AAW49123 Rat GABABR1b prote
21	2023.5	46.3	960	20	AAW28841 Rat GABABR1a recep
22	2023.5	46.3	960	20	AAW49122 Rat GABABR1a prote
23	2023.5	46.3	960	22	AAB50089 Murine GABA-B-R1a.
24	1967	45.0	886	20	AAW14110 Human GABAB recept
25	1721	39.3	753	22	AAB50093 GBL protein. Caen
26	1290	29.5	941	20	AAW29796 Human gamma-amino-
27	1290	29.5	941	21	AAW90938 Human GABA-B recep
28	1290	29.5	941	21	AAW51928 Human GABA-B recep
29	1290	29.5	941	21	AAW70328 Human GABA-B-R2 re
30	1290	29.5	941	21	AAW79202 Human GABAB recept
31	1290	29.5	941	21	AAW44342 Human gb2 GABA B r
32	1290	29.5	941	22	AAB50088 HG20 protein seque
33	1290	29.5	943	20	AAW28837 Human GABABR2 rece
34	1289	29.5	941	21	AAW68743 A human gamma-amin
35	1287	29.4	940	21	AAW44343 Rat gb2 GABA B rec
36	1285.5	29.4	914	21	AAW44344 Protein-1 related
37	1285.5	29.4	965	21	AAW44345 Protein-2 related
38	1285	29.4	1303	20	AAW49132 GABA-BR2*Gqo5 fusi
39	1284	29.4	898	20	AAW14082 Human GABABR2 prot
40	1284	29.4	898	21	AAW70326 Human gamma amino
41	1283	29.3	940	21	AAW90937 Rat GABA-B recepto
42	1283	29.3	940	21	AAW70327 Rat gamma amino bu
43	1282	29.3	940	21	AAW51927 Rat GABA-B recepto
44	1263	28.9	883	20	AAW14081 Rat GABABR2 protei
45	1249.5	28.6	473	20	AAW49107 Human GABABR1b ext

ALIGNMENTS

RESULT	1
AAB86159	standard; Protein; 840 AA.
ID	AAB86159 standard; Protein; 840 AA.
XX	
AC	AAB86159;
XX	
DT	03-AUG-2001 (first entry)
XX	
DE	D. melanogaster GABA-B receptor protein SEQ ID 2.
XX	
KW	GABA-B receptor; fruitfly; gamma-aminobutyric acid B receptor;
KW	insecticide; transgenic invertebrate; plant protection agent;
KW	human medicine; veterinary medicine; insect.
XX	
OS	Drosophila melanogaster.
XX	
PN	DE19955408-AA1.
XX	
PD	23-MAY-2001.
XX	
PF	18-NOV-1999; 99DE-1055408.
XX	
PR	18-NOV-1999; 99DE-1055408.
XX	
PA	(FARB) BAYER AG.
XX	
PI	Raming K, Mezler M, Mueller T;
XX	
DR	WPI: 2001-318282/34.
DR	N-PSDB; AAH20519.
XX	
PT	New invertebrate gamma-aminobutyric acid receptor proteins, useful in screening for potential insecticides, for plant protection or medicine, also related nucleic acid

XX Claim 2: Page 16-21; 62pp; German.
XX This invention describes a novel polypeptide (I), functioning as a
CC gamma-aminobutyric acid -B (GABA-B) receptor which has insecticidal
CC activity. (I), also the nucleic acid (II) that encodes it and related
CC vectors, host cells, antibodies and transgenic invertebrates, are used
CC for identifying: (i) new plant protection agents, i.e. modulators of (I)
CC with insecticidal activity, which may also be useful in human or
CC veterinary medicine; and (ii) genes that encode polypeptides involved in
CC assembly of functionally related GABA-B receptors in insects. This
CC assemblage represents a fruitfly (*Drosophila melanogaster*) GABA-B receptor
CC which is described in the method of the invention.
XX
SQ Sequence 840 AA:

Query Match 100.0%; Score 4374; DB 22; Length 840;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 840; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MRKDMTSDGAVTFWIFLLCLLIAGPHLQGGVAGRPDELHIGIIPPIAGKGGOGGACMPA 60
Db 1 mrkdmtsdgavtfwifllclliaspghlqggvagrpdelhigifpiagkggwgqggacmpa 60

Qy 61 TRALDDVNKQPNLPGFKLILHSNDECEPGLGASVYNNLLYKPKQLMLLAGCSTVCT 120
Db 61 tralddvnkqpnlpfgkllilhsndecepglgasvymynllnkpqkmlilagcstvct 120

Qy 121 TVAEAAKMNLLIVLCYGASSPALSDRKRFPTLFRTHPSATVHNPTRIKLMKKFGWSRVAI 180
Db 121 tvaeaaakmnllivlcygasspalsdrkrfptlfrthpsatvhnptriklmkkfgwsrva 180

Qy 181 LQAEVEFVISTVEDLENRCMEAGVEIVTROSEFLSDPTDVAVRNLRRODARIIVGLFYVAA 240
Db 181 lqaevefivistvedlenrcmeagveivtrdsflsdptdavrnlrrrdarivglfyvaa 240

Qy 241 RRVLCEMYKOOLYGRAHVPWFIFGWEDNWEVNLKAEGITCTVEOMRTAAEGHLLTTEALM 300
Db 241 rrvlcemykoolygrahvpwfifgwyednwevnlkaegitctveqmrtaaeaghllttealm 300

Qy 301 WNONNOTTISGMTAEERHRLNQAILEEGYDINHRYPEGYQAEPLAYDAVWSVALAFNK 360
Db 301 wnqnnqttisgmtaeerhrlnqaileegydinhdrypegyqaeplaydavwsvalafnk 360

Qy 361 TMERLTGKSLDFYTTDKIEADEIYAANNSTQFLVSGVWAFSSOGDRIALQIOMI 420
Db 361 tmerltgkksldfyttdkieadeiyaannstqflvsgvwwafssogdrialtqieqmi 420

Qy 421 DGKYEKLYGYDTOLDNLWSLNTQWIGGKVPQDRTIVTHVLTSLPLFCVMCHTSSCGI 480
Db 421 dgkyeklygydytoldnlswlntqwiggvkvpqdrtiwthvltvslplfvcmtctisscg 480

Qy 481 FVAFALIIFNIMNKHRRVIOSSHPVCNTIMLFGVILCLISVILGIDGRFVSPEEYKIC 540
Db 481 fvafaliiifnwnkhrrviqsshpvcntimlfgviliiclisvillgidgrfvspeeypkic 540

Qy 541 QARAWLLSTGFTLAYGAMFSKVRVHRFTTKAKTDPKKVPKLYTWVSGLLSIDLVIL 600
Db 541 qarawllstgftlaygamfsvkrvrhrfttkaktdpkkvpklytwvsgllsidlvil 600

Qy 601 LSWQIFDPLQRYLETTPLEDVPSTDDIKIRPELEHCESONSMWGLVYFGKGLILVFG 660
Db 601 lswqifdplqrylettpledvpstddikirpelehesonsmwglvyfgkglilvfg 660

Qy 661 LFLAYETRSIKVKQINDSRVVGMSIYNVWVLCITAPVGMVIAISOQDASFAVALAVIFC 720
Db 661 lflayetrsikvkqindsrvgmsiynvwlclitapvgmviasoqdasfavalavifc 720

Qy 721 CFLSMILLIFVPKVIETIRHPKDAESKYNPDSDAISKEDEERYKLVITENEOLRLITQKE 780
Db 721 cflsmillifvpkvieltrhpkdskynpdpsaiskederyklviteneolrlitqke 780

Qy 781 EKIRVLRORLYVERGDAGKTELGATGVASAAVAVTTSQPASLINSSAHATPAATLAIQTGE 840
Db 781 ekirvlrqlrlyvergdagktelngatgvasaavattsqpaslinssahatpaatlaigtge 840

RESULT 2
AAW40119 standard; Protein; 844 AA.
XX AAW40119;
XX 03-JUN-1998 (first entry)
XX Human GABA-BR1b receptor protein.
XX Gamma-aminobutyric acid; GABA-BR1a/b receptor; human; brain; agonist;
KW inhibitory neurotransmitter; peripheral nervous system; antagonist;
KW treatment; dementia; depression; anxiety; bronchial inflammation; asthma;
KW epilepsy; cognitive function.
XX Homo sapiens.
XX OS
XX WO9746675-A1.
XX 11-DEC-1997.
XX 19-MAR-1997; 97WO-EP01370.
XX 22-NOV-1996; 96US-0756091.
XX 30-MAY-1996; 96US-0655716.
XX (NOVS) NOVARTIS AG.
XX Bettler B, Bittiger H, Froestl W, Kaupmann K, Mickel SJ;
XX WPI; 1998-042183/04.
XX N-PSDB; AAV10267.
XX Purified GABA-B receptor or receptor protein - and antagonists of
XX these which may be useful in treating nervous system disorders
XX Claim 4; Page 86-90; 108pp; English.
XX This sequence represents a novel human GABA-B receptor protein,
XX GABA-BR1b. GABA (gamma-aminobutyric acid) is the major inhibitory
XX neurotransmitter found in the brain and peripheral nervous system
XX and this receptor may be used for the identification of GABA-B
XX receptor agonists and antagonists. Such proteins may be used in
XX treatment of dementia, depression, anxiety, epilepsy, spasticity,
XX bronchial inflammation or asthma or to improve cognitive function.
XX GABA-B receptor ligands and probes derived from this sequence can be
XX used to assay for GABA-B receptors or DNA encoding them.
XX
SQ Sequence 844 AA;

Query Match 46.5%; Score 2035; DB 19; Length 844;
Best Local Similarity 49.3%; Pred. No. 7.5e-193;
Matches 387; Conservative 151; Mismatches 219; Indels 28; Gaps 9;

Qy 23 SPHL---OGVACRPDE----LHIGIFPIAGKGGOGGACMPATRLALDDVNKPNLL 75
Db 32 sphlprhsrvpphserravvialfpm--gwpqggacqpvameadvnrrdil 89

Qy 76 PGFKLILHSNDECEPGLGASVYNNLLYKPKQLMLLAGCSTVCTTVAAKMNLLIVLC 135
Db 90 pdeylklilhsdskdpqgqetkyllylndypkiliimpocssvstlvaearmnlvls 149

Qy 136 YGASSPALSDRKRFPTLFRTHPSATVHNPTRIKLMKKFGWSRVAIILQAEVEFISTVEDL 195
Db 150 ygasspalsnrqrfptlfrthpsatvhnptriklmkkfgwsrvaifekwgkktatqgtftstldl 209

Qy 196 ENRCMEAGVEIVTROSEFLSDPTDVAVRNLRRODARIIVGLFYVAAARRVLCENKQOLYGR 255

Db 210 eervkeagieitfrqsfpsdpvknkqdarilvglyfetearkvfcvkerlfgk 269
QY 256 AHVWFFIGWEDNWEVNLKAEIGTCTVEQMRIAEAGHLTEALMWNQNTTISGMTAE 315
Db 270 kyvwfligwyadnwfk1--ydpnsinctvdeanteaveghitteivmlpantrsisnmtsq 327
QY 316 EFRHRLNQAIEEGYDINHRYPE---GYQEAFLAYDAVMSVALAFNKTHERLTGKKSL 372
Db 328 efvektkrl-----krhpeetggfqaepplaydaiwalalaloktsggggrsgvrl 378
QY 373 RDTYTDKEIADEIYAAMNSTQFLGVSVAFSSQGDRIALTQIEQMDGKYEKLGYDT 432
Db 379 edfynnnqitdqiyrannsssfegvghvfdasgrmawtlieqlggysykgiyyds 438
QY 433 QLDNLSWLNTEQWIGKVPQDRTIVTHVRLTVSLPLFVCMCTTSSCGIFVAFALIENIW 492
Db 439 tkddlsksktkwiggspadqtlviktfrflsqklfisvsvlsslgivlavvcslfniy 498
QY 493 NKHRRVIOSSHPCVNTIMLFGVVICLISVILLGIDGRFVSPEEYPKICQARAWLLSTGFT 552
Db 499 nshvryiqnsqpnlnltavgcslalaavfplgldgyhigrngpfvcqarlwlgfsg 558
QY 553 LAYGAMFSKVRVHRFTTK--AKTDPKKVPEPKLYTMVSGLLSIDLVILLSSQIFDPLQ 610
Db 559 lgygsmftkiwwhtvftkkekewrktlepklyatvgllvgmdvltaiwqivdplh 618
QY 611 RYLETFPLEDPVSTDDIKIRPELEHCEQSQRNSMMGLVYGFKGLIILVFLFLAYETRSI 670
Db 619 rtietfakeepkedi-dvslilpqlehcscrkmtwtgifygkglllllglflayetsk 677
QY 671 KVKQINDSRVYVMSIYNVVVLCITAPVGMVIAQQDASFAFVALAVIFCCFLSMLIFV 730
Db 678 stekindhavgmaliynvavlitapvtmilssqgdaafafaslaivfssyitlvvlv 737
QY 731 PKVIEVIRHP--KDKAESKYNPDASISKEDEERYQKLVTEQOLRLITQEEKIRVLQ 788
Db 738 pkmrilrtgwgseqadtmtgtsstnnneeksrllekenrelekiiaekeervselrh 797
QY 789 RLVR 793
Db 798 qlqsr 802
RESULT 3
ID AAY28839
XX AAY28839 standard; Protein; 844 AA.
AC AAY28839;
XX 17-JAN-2000 (first entry)
DE Human GABABR1b receptor protein.
XX
KW GABABR1b receptor protein; cloning; rat brain; GABABR2; GABAB receptor;
KW human gamma-aminobutyric acid receptor; metabotropic receptor; screening;
KW synaptic transmission; GABABR1b; cloned receptor; splice variant;
KW modulatory agent; molecular activity assay; antispastic; anti-addictive;
KW antineurodegeneration; analgesic; cardiovascular activity.
OS Homo sapiens.
XX
PN W09951636-A2.
XX
PD 14-OCT-1999.
XX
PF 02-APR-1999; 99WO-US07352.
XX
PR 03-APR-1998; 98US-0080676.
XX
PA (NP5P-) NPS PHARM INC.
XX
PI Garrett JE, Simin RT, Busby JG, Stormann TM;

XX WPI: 1999-610994/52.
DR N-PSDB: AAX90921.
XX
PT Novel nucleic acids, used to screen for specific modulators, e.g. for
PT treating spasticity or Alzheimer's disease -
XX
PS Disclosure; Fig 2A-2E; 78pp; English.
XX
CC The present sequence encodes GABABR1b receptor protein cloned from rat
CC brain. This is closely related to GABABR2. GABAB receptors are
CC metabotropic receptors that modulate synaptic transmission in brain.
CC GABABR1a differs from GABABR1b in that the N-terminal 147 residues are
CC replaced by 18 amino acids. Both of these cloned receptors appear to be
CC splice variants. They are expressed in cells that express GABABR2. This
CC nucleotide sequence is used to screen for specific modulators. These
CC modulators have antispastic, antineurodegeneration, analgesic, anti
CC -addictive, cardiovascular activities.
CC Note: SEQ ID NO. 8 is referred as the GABABR1a receptor protein in
CC the specification.
XX
SQ Sequence 844 AA;
Query Match 46.5%; Score 2035; DB 20; Length 844;
Best Local Similarity 49.3%; Pred. No. 7.5e-193;
Matches 387; Conservative 151; Mismatches 219; Indels 28; Gaps 9;
QY 23 SPHL---QGVAGRPDE---LHIGGIPIAGKGGQGGQACMPATRLALDDVNKQPNLL 75
Db 32 sphlprhsrvpphserravyigalfpms--ggwp9ggagcqvamaledvnsrrdl 89
QY 76 PGFKLILHSNDECEPGLGASVWYNNLLNKPQKMLLAGCSTVCTTVAEAAKMWNLIVLC 135
Db 90 pdyelkllhdsckdpqatkylyellyndpikilimpqcssvstlvaeamwllvlis 149
QY 136 YGASSPALSDRRKPTLFTPHSATVHNPTRIKMKKGSVRVAILQAAEEVFSTVEDL 195
Db 150 ygsspsalsnqrftfrthpsatlhnptrvklfekgwkkiaitqgtteftstldld 209
QY 196 ENRCMEAGVEIVTQSFSLSDPTDAVNRILRQDARILVGLFYVVAARRVLCENYKQOLYGR 255
Db 210 eervkeagieitfrqsfpsdpvknkqdarilvglyfetearkvfcvkerlfgk 269
QY 256 AHVWFFIGWEDNWEVNLKAEIGTCTVEQMRIAEAGHLTEALMWNQNTTISGMTAE 315
Db 270 kyvwfligwyadnwfk1--ydpnsinctvdeanteaveghitteivmlpantrsisnmtsq 327
QY 316 EFRHRLNQAIEEGYDINHRYPE---GYQEAFLAYDAVMSVALAFNKTHERLTGKKSL 372
Db 328 efvektkrl-----krhpeetggfqaepplaydaiwalalaloktsggggrsgvrl 378
QY 373 RDTYTDKEIADEIYAAMNSTQFLGVSVAFSSQGDRIALTQIEQMDGKYEKLGYDT 432
Db 379 edfynnnqitdqiyrannsssfegvghvfdasgrmawtlieqlggysykgiyyds 438
QY 433 QLDNLSWLNTEQWIGKVPQDRTIVTHVRLTVSLPLFVCMCTTSSCGIFVAFALIENIW 492
Db 439 tkddlsksktkwiggspadqtlviktfrflsqklfisvsvlsslgivlavvcslfniy 498
QY 493 NKHRRVIOSSHPCVNTIMLFGVVICLISVILLGIDGRFVSPEEYPKICQARAWLLSTGFT 552
Db 499 nshvryiqnsqpnlnltavgcslalaavfplgldgyhigrngpfvcqarlwlgfsg 558
QY 553 LAYGAMFSKVRVHRFTTK--AKTDPKKVPEPKLYTMVSGLLSIDLVILLSSQIFDPLQ 610
Db 559 lgygsmftkiwwhtvftkkekewrktlepklyatvgllvgmdvltaiwqivdplh 618
QY 611 RYLETFPLEDPVSTDDIKIRPELEHCEQSQRNSMMGLVYGFKGLIILVFLFLAYETRSI 670
Db 619 rtietfakeepkedi-dvslilpqlehcscrkmtwtgifygkglllllglflayetsk 677
QY 671 KVKQINDSRVYVMSIYNVVVLCITAPVGMVIAQQDASFAFVALAVIFCCFLSMLIFV 730

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Db 678 stekindhvragmaiynvavclitapvtmllsqgdaafafaslaivfssyilvifv 737
QY 731 PKVIEVIRHP--KDKAESKYNPDSAISKEDEERYQKLVTENEQLQRLITQKEEKIRVLQ 788
Db 738 pkmrrlitrgewqseagdtmktgssntnnneeksrlllekenrelekliaeekeervselrh 797
QY 789 RLVER 793
Db 798 qlqsr 802

RESULT 4
ID AAY14102 standard; Protein; 844 AA.
AC AAY14102;
XX
XX
DT 21-JUL-1999 (first entry)
XX
DE Human GABAB receptor lb protein sequence.
XX
KW GABAB receptor; gamma aminobutyric acid type B receptor; inhibitor;
KW transient lower oesophageal sphincter relaxation; spasticity; emesis;
KW gastro-oesophageal reflux disease; epilepsy; psychiatric disorder; TLESR;
KW irritable bowel syndrome; dyspepsia; arthritis; allergy; diagnosis;
KW autoimmune disease; neoplastic disease; infectious disease; therapy.
XX
OS Homo sapiens.
XX
XX WO9921890-AL.
PN
PD 06-MAY-1999.
XX
XX 27-OCT-1998; 98WO-SF01947.
XX
PR 17-JUL-1998; 98SE-0002575.
PR 27-OCT-1997; 97SE-0003914.
PR 16-MAR-1998; 98SE-0000864.
XX
XX (ASTR ) ASTRA AB.
XX
XX Ekstrand J;
PI
XX
XX WPI; 1999-302985/25.
DR
DR N-PSDB; AAX58055.
XX
XX Polynucleotides encoding human and canine gamma aminobutyric acid
PT type B receptors, used to screen for compounds that are inhibitors
PT of transient lower oesophageal sphincter relaxations
XX
PS Claim 17; Page 90-94; 222pp; English.
XX
XX This sequence is a human gamma aminobutyric acid type B (GABAB)
CC receptor of the invention. Nucleic acid molecules encoding GABAB
CC receptors can be used to screen for compounds that are inhibitors of
CC transient lower oesophageal sphincter relaxations (TLESR). They can also
CC be used to screen for agonists or antagonists of the GABAB receptors.
CC Inhibitors of TLESR are useful for treating gastro-oesophageal reflux
CC disease. Other uses of GABAB receptors, such as human GABAB R1c or 1d,
CC comprise diagnosis or treatment of conditions related to GABAB
CC dysfunction, e.g. epilepsy, psychiatric disorders, emesis, irritable
CC bowel syndrome, dyspepsia, spasticity, arthritis, allergies, autoimmune
CC diseases, neoplastic diseases, pain and infectious disease.
XX
SQ Sequence 844 AA;

Query Match 46.5%; Score 2035; DB 20; Length 844;
Best Local Similarity 49.3%; Pred. No. 7.5e-193;
Matches 387; Conservative 151; Mismatches 219; Indels 28; Gaps 9;
QY 23 SPHL---QGVAGRPFDE----LHIGGIFPIAGKGGWGGQACMPATRLALDQVKNQPNLL 75

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Db 32 sphlprphsrpvpshsserravyigalfpms--gwpvggacqavamealedvnrdil 89
QY 76 PFGKILILHSNDSECPGLGASWYMLLYNKPQKLKLAGCSTVCTTVAFAAKWNLIVLC 135
Db 90 pdyelkllhdsckdpqgatkyllyellyndpikilimpqgssvstlvacaarmnllivls 149
QY 136 YGASSPALSDKRPFPTLFRTHPSATVHNPTRIKLMKFKQWSRAILQQAEEVFISTVEDL 195
Db 150 ygssspalsnqrfrptfrthpsatlhmptrvklfekgwkkkatiqgtteftstldl 209
QY 196 ENRCMEAGVEIVTRQSFSLSDPTDAVNLRQDARIIVGLFVYVAARRVCEWYKQOLYGR 255
Db 210 eervkeagleitfrqsfdsdpavpknkrqdarliivgifyetearkvfveykerlfdk 269
QY 256 AHVWFFIGWYEDNWYEVNLKABGICTVBQMRIAEGHLLTTEALMWNQNNQTTISGMTAE 315
Db 270 kyvfwlgyadnwfkf--ydpstinctvdemteaveghitteivmlnpantrsismtsq 327
QY 316 EFRHLNQAALIEEGYDINHRYPE---GYOEAPLAYDAYMSVALAFNPKTMERLTGKKSL 372
Db 328 efvekltkrl-----krhpeetggfgeaplaydaiwalalalnktsggggrsgvrl 378
QY 373 RDTTDTDEIADEIYAAMNSTQFLGSGVAVFSSQGDRIALTQIEQMDCKVEKIGYYDT 432
Db 379 edfnynndqitdqiyramsssfegvshvfdasgrmawtllieqlqggykkigyds 438
QY 433 QLDNLISWLTQWIGGKVPQDRITVTHVLTVSPLFVCMCTISSCGIFVAFALIFNFW 492
Db 439 tkddlsawktdkwigsgppadqclvktffisqklfsvsvlsslgvlavvcfsfnly 498
QY 493 NKHRRVIOSSHPVCNTIMLFGVILISVILGIDGRFVSPBEYPRKICQARAWLLSTGFT 552
Db 499 nshvryiqnsqpnlnltavgcslalavfplgldyhgirngqpfvcqarlwlglgfs 558
QY 553 LAYGAMFSKVMVRHREPTTK--AKTDPKKKVEPWKLYTWVSGLLSIDLVILLSQWIPDPLQ 610
Db 559 lgygsmfktkwvhtvftkkekewrktlepwklyatvgllivgmdvltlaiwqivdplh 618
QY 611 RYLETFPLEDPVSTTDDIKIRPELEHCEQSQRNSMWGLVYGPGLLVFLGLFLAYETRSL 670
Db 619 rtiefakeepkedl-dvsilpqlehcscrkmtwtgifygk9lililgifylvetksv 677
QY 671 KVKQINDSRVGSINVVVLCILITAPVGMVIAQQDASFAFVALAVIFCCFLSMLLIFW 730
Db 678 stekindhvragmaiynvavclitapvtmllsqgdaafafaslaivfssyilvifv 737
QY 731 PKVIEVIRHP--KDKAESKYNPDSAISKEDEERYQKLVTENEQLQRLITQKEEKIRVLQ 788
Db 738 pkmrrlitrgewqseagdtmktgssntnnneeksrlllekenrelekliaeekeervselrh 797
QY 789 RLVER 793
Db 798 qlqsr 802

RESULT 5
ID AAY32467 standard; Protein; 844 AA.
XX
XX AAY32467;
XX
XX 27-MAR-2000 (first entry)
XX
XX Human G-protein coupled receptor GABAB1b.
XX
KW GABAB1b; G-protein coupled receptor; human; antibacterial;
KW antiviral; virucide; antiparasitic; analgesic; cytostatic;
KW antidiabetic; anorectic; cardiant; antiparkinsonian;
KW hypertensive; hypotensive; antiemetic; osteopathic; antianginal;
KW cerebroprotective; antitumor; antiallergic; neuroleptic;
KW tranquilizer; antidepressant; nootropic; antimigraine;
KW anticonvulsant; neuroleptic; agonist; antagonist; inhibitor;

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therapy; diagnosis.
 Homo sapiens.
 WO9958567-A1.
 18-NOV-1999.
 03-MAY-1999; 99WO-US09655.
 08-MAY-1998; 98US-0075463.
 (SMIK) SMITHKLINE BEECHAM CORP.:
 Elshourbagy NA, Halsey WS;
 WPI; 2000-116287/10.
 N-PSDB; AA235410.
 New human GABABb polypeptides and polynucleotides used to identify
 agonists, antagonists and inhibitors for use in therapy
 Claim 1; Page 35-41; 46pp; English.
 This amino acid sequence represents the human G-protein coupled
 receptor GABABb, as deduced from an isolated brain cDNA clone
 (see AA235410). The invention provides GABABb polypeptides and
 polynucleotides, and methods for producing such polypeptides by
 recombinant methods. GABABb polypeptides may be used for
 identifying agonists and antagonists/inhibitors, and for detecting
 diseases associated with inappropriate GABABb activity or levels.
 GABABb polypeptides and polynucleotides, agonists, antagonists and
 antibodies are used to treat bacterial, fungal, protozoan and viral
 infections, particularly HIV-1 and HIV-2, pain, cancer, diabetes,
 obesity, anorexia, bulimia, asthma, Parkinson's disease, acute
 heart failure, hypotension, hypertension, urinary retention,
 osteoporosis, angina pectoris, myocardial infarction, stroke,
 ulcers, allergies, benign prostatic hypertrophy, migraine,
 vomiting, psychotic and neurological disorders including anxiety,
 schizophrenia, manic depression, depression, delirium, dementia and
 severe mental retardation, and dyskinesias such as Huntington's or
 Gilles de la Tourette's syndrome.
 Sequence 844 AA;
 Query Match 46.5%; Score 2035; DB 21; Length 844;
 Best Local Similarity 49.3%; Pred. No. 7 5e-193;
 Matches 387; Conservative 151; Mismatches 219; Indels 28; Gaps 9;
 23 SPHL---QGGVAGRPE-----LHIGGIFPIAGKGGGGOACMPATRLALDDVKNQPNLL 75
 32 sphlprphsrpvpsserravyigalfpms--ggwpgggacqpavemaledvnsrrdl 89
 76 PGFKLLHSNDSECEPGLGASVWYNLLYKPKQLMLLAGCSTVCTTVAEAKWNLIVLC 135
 90 pdyelklhndskcdpggqtkyllyellyndpikilmpgcsvstlvaearmwnliivs 149
 136 YGASSPALSDRKRFPPTLFRTHPSATVHNTRIKLMKFGWSRVAILQQAEEVFISTVEDL 195
 150 yssspalsnrgfpffrthpsatlmprvklfkewgkktatqgttevtfstldd 209
 196 ENRCMEAGVEIVTROSFLSDPTDAVNLRRQDARIIVGLFYVVAARRVLCMEYKQOLYGR 255
 210 eervkeagleitfrqsfspavpknkrqdariivglfytearkvfcvvykerlfgk 269
 256 AHVWFEGWEDNTEVNLKAGITCTVQMRITAEAGHLTTEALMMNNQNTTISGWTAE 315
 270 kyvwfligwyadnwfkii--ydpisinctvtemteaveghittelmvlnpantrsisnmts 327
 316 EFRHRLNALIEEGYDINHRYPE---GYOEAPLAYDAVMSVALAFNKTKERLTGKSL 372
 328 efvekitkrl-----krhpeetggfqaepalaydaiwalainktsggggrsgvrl 378

Qy 373 RDTYTDKEIADEIYAAMNSTOFLGVSQVAFSSOGDRIALQIQEOMIDGKYEKLGYYDT 432
 Db 379 edfnynnqtitdqiyramsssfegvghvfdagarmawtlieqlggsgykkgydds 438
 Qy 433 QLDNLSWLNTEQWIGKVPQDRFTIVTHVLRTVSLPLFVCMCTISSCGIFVAFALIFNIW 492
 Db 439 tkddlsksktkwiggspadqtlvktfrflsklfisvslsslgvlavvcisfnly 498
 Qy 493 NKHRRVIOSSHVPVCMTIMLFGVVICLISVILLGIDGRFVSPEEYPKICOARAWLLSTGFT 552
 Db 499 nshvryiqnsqpnlnltaavgcsalaaavfplgldghyhnrgqpfvqcqarlwlglgfs 558
 Qy 553 LAYGAMFSKVMVRHRTTK--AKTDPKKVBPWKLYTWVSGLLSIDLVLLSQWIFDPLQ 610
 Db 559 lgygsmfkikwvhtvftkkekewrktlepkkiyatvgllvgmdivclaiwqivdph 618
 Qy 611 RYLETFFLEDVPTTDDIKIRPELEHESQSRNSMMLGVYFGKGLTVFLGFLAYETRSI 670
 Db 619 rtietfakeepkedl-dvsiilpqlehcscrkmtwtlgyfygklllllgliflayetksv 677
 Qy 671 KVKQINDSRYVGMSTYNNVVVLCITAPVGMVITASODASFAFVALAVIFCCFLSMLLIPV 730
 Db 678 stekindhvrgmaiynvavlicltapvtmilssqgdaafaslaivfssyitlvvlfv 737
 Qy 731 PKVIEVIRHP--KDKAESKYNPDSAISKDEERYOKLVTENEQLQRLITQKEKIRVLRQ 788
 Db 738 pkmrllirgwgseqadmtkgsstnnneeksrllckenrelekilaekervseirh 797
 Qy 789 RLVER 793
 Db 798 qlqr 802
 RESULT 6
 AAY14107
 ID AAY14107 standard; Protein; 899 AA.
 AC AAY14107;
 XX
 DT 21-JUL-1999 (first entry)
 XX
 DE Human GABAB receptor le protein sequence.
 XX
 KW GABAB receptor; gamma aminobutyric acid type B receptor; inhibitor;
 KW transient lower oesophageal sphincter relaxation; spasticity; emesis;
 KW gastro-oesophageal reflux disease; epilepsy; psychiatric disorder; TLESR;
 KW irritable bowel syndrome; dyspepsia; arthritis; allergy; diagnosis;
 KW autoimmune disease; neoplastic disease; infectious disease; therapy;
 KW alternative splicing; isoform.
 XX
 OS Homo sapiens.
 XX
 PN WO9921890-A1.
 PD 06-MAY-1999.
 XX
 PF 27-OCT-1998; 98WO-SE01947.
 XX
 PR 17-JUL-1998; 98SE-0002575.
 PR 27-OCT-1997; 97SE-0003914.
 PR 16-MAR-1998; 98SE-0000864.
 XX
 PA (ASTR) ASTRA AB.
 XX
 PI Ekstrand J;
 XX
 DR WPI; 1999-302985/25.
 DR N-PSDB; AAX58062.
 XX
 PT Polynucleotides encoding human and canine gamma aminobutyric acid
 PT type B receptors, used to screen for compounds that are inhibitors
 PT of transient lower oesophageal sphincter relaxations

Qy	191	TVELENRCMEAGVIEIVTRQSFLSDPTDAVRNLRRODARIILVGIFYVAARRVLCEMYKQ	250
Dd	205	tlddleervkkeagieltfrqsfspavpvknkrqdariilvgfyetearkvfveyke	264
Qy	251	OLYGRAHWFFIGWYEDNWYEVNLKAEGITCTVEOMRIRAEGLHTEALMWNQNQTIS	310
Dd	265	rllfkkyvfwllygadowkft--ydpnsinctveenteaveghitfeimlnpantrs	322
Qy	311	GMTAEFRHLRNOALTEGYDINHORYPE--GYOEAPLAYDAVWSVALAFNKTMERLTT	367
Dd	323	nmtsqefvekltkrl-----krhpeetggfqeaplaydaivalalalnhtsggggr	373
Qy	368	GKSLRDFTYTDKEIADEIYAAMNSTQF LGVGVVAFFSQGDRIALTQIBQMIDGKYEK	427
Dd	374	sgvrledfnynnqtldgiyramnsssfegsvghvvfdasgrmawtlieqlgggsyki	433
Qy	428	GYDTOLDNLSWLNETEOWIGKGVPQDRRTIVTHLVRFVSUPLFCVMCTISSCGFI	487
Dd	434	gyydstkdllswsktdkwiggppadqtiivtkfrflsqklfisvsavlslglavvcl	493
Qy	488	IFNIWNKHRRVIQSSHPCVNTIMLFQVVICLSVILLGIDGRVSPPEEPKICQAARALL	547
Dd	494	sfnlyshrvryiqnsgpnlnltavgcsialaaavplgidgyhigrsqffvcqarlwl	553
Qy	548	STGTFLAYGMFSKVRYRHRETK--AKTDPKKKPWKLYTMVSGLLSIDLVILLSMQI	605
Dd	554	glgfslygysmfkiwwhtvtkkkeekewrktlepwklyatvgllvgmdvltlaiwqi	613
Qy	606	FDPLORYLETPLEPDPVSTDIDIKRPELEHCESQRNSMWLGVLVYGFKGLILVFGL	665
Dd	614	vdpilhrtietakeepkedi-dvsilpqlehcscskmntwlgfyfykgllillgilay	672
Qy	666	ETRSIKVKQINDSRVGVGSINYNVVLCITAPVGMVIAEQODASFAFVALAVFCFLSM	725
Dd	673	eksvstekindhraqvmaynavvlciltapytmllssqqdaafaslaivfssyitl	732
Qy	726	LLIFVPKVIEWIRHPDKAESK--YNPDSAISKEDEREYQKLVTENEQLRLITQREEKI	783
Dd	733	vvlfpkmrrlitrgewsetqdtmktgstnnneeksrllekenrelekiiaeeerv	792
Qy	784	RVLQRQLVER	793
Dd	793	selrhqlqsr	802
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RESULT 8			
AAV14105	ID	AAV14105 standard; Protein; 964 AA.	
XX	AC	AAV14105;	
XX	CC		
XX	DD		
DT	21-JUL-1999	(first entry)	
XX	XX		
XX	XX	Canine GABAB receptor la protein sequence.	
KW	GABAB receptor; gamma aminobutyric acid type B receptor; inhibitor;		
KW	transient lower oesophageal sphincter relaxation; spasticity; emesis;		
KW	gastro-oesophageal reflux disease; epilepsy; psychiatric disorder; TLESR;		
KW	irritable bowel syndrome; dyspepsia; arthritis; allergy; diagnosis;		
KW	autoimmune disease; neoplastic disease; infectious disease; therapy.		
OS	Canis familiaris.		
XX	XX		
PN	WO9921890-A1.		
XX	XX		
PD	06-MAY-1999.		
XX	XX		
PF	27-OCT-1998; 98WO-SE01947.		
XX	XX		
PR	17-JUL-1998; 98SE-0002575.		
PR	27-OCT-1997; 97SE-0003914.		
PR	16-MAR-1998; 98SE-0000864.		

XX	(ASTR) ASTRA AB.
PA	Ekstrand J;
XX	
PI	WPI; 1999-302985/25.
DR	N-PSDB; AAX58056.
XX	
PT	Polynucleotides encoding human and canine gamma aminobutyric acid
PT	type B receptors, used to screen for compounds that are inhibitors
PT	of transient lower oesophageal sphincter relaxations
XX	
PS	Claim 17; Page 99-105; 22pp; English.
XX	
CC	This sequence is a canine gamma aminobutyric acid type B (GABAB)
CC	receptor of the invention. Nucleic acid molecules encoding GABAB
CC	receptors can be used to screen for compounds that are inhibitors of
CC	transient lower oesophageal sphincter relaxations (TLRSR). They can also
CC	be used to screen for agonists or antagonists of the GABAB receptors.
CC	Inhibitors of TLRSR are useful for treating gastro-oesophageal reflux
CC	disease. Other uses of GABAB receptors, such as human GABAB Ric or ld,
CC	comprise diagnosis or treatment of conditions related to GABAB
CC	dysfunction, e.g. epilepsy, psychiatric disorders, emesis, irritable
CC	bowel syndrome, dyspepsia, spasticity, arthritis, allergies, autoimmune
CC	diseases, neoplastic diseases, pain and infectious disease.
XX	
SQ	Sequence 964 AA;
	Query Match 46.4%; Score 2031.5; DB 20; Length 964;
	Best Local Similarity 49.4%; Pred.No. 2.1e-192;
	Matches 386; Conservative 152; Mismatches 216; Indels 27; Gaps
Qy	24 PHLOGGVAGRPDE-----LHIGGIPIAGKGGWGOGACMPATRLADDVYNKPNLLPGFK 79
Db	: : : : : : : : : : : : :
158	phcq--vsrtphserravygaifpms--ggwpggacqpavemaiedvnrrdiilpdye 213
Qy	80 LILHSNDSECEPGLGASVTNLIYNPQKLMLLAGSGTCTVTTVAEAAKWNLIIVLCYGAS 139
Db	: : : : : : : : : : : : :
214	lklhhdsckdpgqatkyllyllndypikilmpgcsvstlvaeaaarnmnlivsygs 273
Qy	140 SPALSDRRKFPTLPRTPHSATVNHPRIKLMKKFGMSRVAILQQOAEVEFTSTVEDLENRC 199
Db	: : : : : : : : : : : : :
274	spalsncrqrfptfrtphsatlnhpvrtvkfkgwrkiatqgttevtftlddleerv 333
Qy	200 MEAGVEIVTRQSFLSDPTDAVRNLRODARIIVGLFVYAARVLCEMYKQOLYGRAHWV 259
Db	: : : : : : : : : : : : :
334	keagieitfrqsffsdpavpvknkqrqdarliiglfyetearkvfcevykerlifgkyvw 393
Qy	260 FFIQWEDNWYEYNLKAEGITCIVEQMRIAEGHLITEALMWNQNQTITISGMTAEFRH 319
Db	: : : : : : : : : : : : :
394	fligwyadnwfk--ydpsinctvdemteaveghitteivmlnpatrslsmtsgefev 451
Qy	320 RLNQALIEGYDINHDPYE---GYOEAPLAYDAVMSVALAFNKMERLTGTCKSLRDFT 376
Db	: : : : : : : : : : : : :
452	kltklr-----krhpetggfqaelaydaivalalalnktsgsgsrgrvledfn 502
Qy	377 YTDKEIADEIYAAMNSTQFLGVSQWAFSSQGDRIALTQIQEMIDGKYEKLGYYDTQLDN 436
Db	: : : : : : : : : : : : :
503	yinnctildqidiramnsstsfegsvghvvfdasgrmarwtlieqlqqsgykkgiydstkd 562
Qy	437 LSWLNTGEOWIGGKVPQDRTIVTHLVTVSLPLFCVMCTISSCGIFVAFALIIFNIWKHR 496
Db	: : : : : : : : : : : : :
563	lswsktdkwlgaggappaqdqtiviktfrfmsqklifisvssissglivlavvcisfnynshv 622
Qy	497 RVIOGSHPVCNTIMLFVICLI SVILLGTDGRFVSPEEPKPCQARALLSTGFTLATG 556
Db	: : : : : : : : : : : : :
623	ryiqsqpnlnhtavcsialaavfpdgdyhgirsqpfvcvcarlwlgfslgy 682
Qy	557 AMFSKVWRVHRFTTK---AKTDPKKKVEPWKLYTWWSGLSISIDLILLSWOIEDFPLORYLE 614
Db	: : : : : : : : : : : : :
683	smfctkivhwtyfckkeekewrktlepwklyttvgllvmqdvltlaiwmqvdpplrtle 742

QY 615 TPLEDPVSTDDIKIRPELEHCSORNSMWLGVLVYGFKGLILVFGFLAYETRISIKVKO 674
 Db 743 tfakeepkedi-dvslpqlehcscskmmtwlgfygkglililgflayetsvstek 801
 QY 675 INDSRYVGSIIYVWVLCITAPVGMVIAQQDASFAFVALAVFCFLSMLLIFVPKVI 734
 Db 802 indhravgmamynvavclitapvtmilsqqdaafaalaivfssyitlvilvfpkmr 861
 QY 735 EVIRHP--KDKASKYNPDSAISKEDERYQKLVTENEQRLRITQKEEKIRVLRQLVE 792
 Db 862 rlitrgewseqdtkmtgstnnneeksrlllekenrelekiiaekervseirhlrs 921
 QY 793 R 793
 Db 922 r 922

RESULT 9
 AAY83145
 ID AAY83145 standard; Protein; 960 AA.
 AC AAY83145;
 DT 24-JUL-2000 (first entry)
 DE Human GABAB1A receptor.
 KW GABAB1A receptor; G-protein; disease; treatment; detection;
 KW therapy; antibody; immune response; infection; cancer; diabetes;
 KW obesity; anorexia; bulimia; Parkinson's disease; heart failure;
 KW hypotension; hypertension; urinary retention; osteoporosis;
 KW angina pectoris; myocardial infarction; stroke; ulcers; asthma;
 KW allergy; benign prostatic hypertrophy; migraine;
 KW neurological disorders including anxiety; schizophrenia;
 KW depression; dementia; Huntington's disease;
 KW Gilles de la Tourette's syndrome.
 OS Homo sapiens.
 XX WO200012106-A1.
 PN 09-MAR-2000.
 PD 30-AUG-1999; 99WO-US19435.
 PF 01-SEP-1998; 98US-0144779.
 PR (SMTK) SMITHKLINE BEECHAM CORP.
 PX Elshourbagy NA;
 PI WPI; 2000-237771/20.
 DR N-PSDB; AA293411.
 XX New GABAB1A polypeptide useful for diagnosis, treatment and prevention
 PT of diseases associated with its expression including infections,
 PT psychotic and neurological disorders and cancer
 PS Claim 1; Page 34-36; 38pp; English.
 CC The GABAB1A receptor is believed to be a member of the GABAB
 CC family of polypeptides. They are therefore of interest because
 CC members of the purinergic 7m receptor family (G-protein coupled
 CC receptors) of genes are involved in a number of biological and
 CC disease manifestations. They are also a successful target for
 CC pharmaceutical intervention. Antibodies directed against GABAB1A
 CC and its peptides can be used to treat bacterial, fungal, protozoan
 CC and viral infections, pain, cancers, diabetes, obesity, anorexia,
 CC bulimia, Parkinson's disease, acute heart failure, hypotension,
 CC hypertension, urinary retention, osteoporosis, angina pectoris,
 CC myocardial infarction, stroke, ulcers, asthma, allergies, benign
 CC prostatic hypertrophy, migraine, vomiting, psychotic and
 CC neurological disorders including anxiety, schizophrenia, depression,

CC dementia and severe mental retardation and dyskinesias such as
 CC Huntington's disease or Gilles de la Tourette's syndrome. The
 CC GABAB1A polypeptide or a vector comprising a sequence encoding the
 CC polypeptide can be used to induce an immunological response in a
 CC mammal to protect against disease. The presence or absence of a
 CC mutation in the nucleotide sequence encoding the GABAB1A polypeptide
 CC can be detected in the genome of a subject and/or the presence or
 CC amount of expression of the polypeptide in a sample from the subject
 CC can be analysed and used to diagnose a disease or susceptibility to a
 CC disease related to the expression or activity of GABAB1A.
 CC Diagnosis can be measured at the RNA level using nucleic acid
 CC amplification, e.g. polymerase chain reaction, RNase protection or
 CC Northern blotting or at the protein level by radioimmunoassay,
 CC competitive-binding assays, Western blot analysis or ELISA assays
 CC (enzyme linked immunosorbent assay).

XX Sequence 960 AA;

Query Match 46.4%; Score 2030.5; DB 21; Length 960;
 Best Local Similarity 49.3%; Pred. NO. 2.6e-192;
 Matches 384; Conservative 152; Mismatches 220; Indels 23; Gaps 8;

QY 24 PHLQGGVAGRPDE--LHIGGIFPIAGKGGWGGQACMPATRLALDDVANKQPNLLPGFKLI 81
 Db 154 phcqvnrtpsherravyigalifpms--ggwpgggcgcqavemaledvnsrrdlpdyelk 211
 QY 82 LHSNDSECEPGLGASVMYNNLKNPKOKLMLLAGCTVCTVTAEEAAKMWNLVLCYGASSP 141
 Db 212 lhhdsckdpqgatkyllyellndpikilmpgcsstclvaeaarmnllvlsygsesp 271
 QY 142 ALSDRKREPTLFRTHPSATVHNPTRIKLMKFGSRVAILQQAEEVFISTVEDLENRCME 201
 Db 272 alsnrqrftfrthpsatlhnptrvkifekwggkikiatqitqtevtftldldservke 331
 QY 202 AGVEIVTQSFLSDPTDAVRNLRPRODARIIVGLFVVAARVLCMYKQOLYGRAHVWF 261
 Db 332 agieitfrqsfdsdpavpvknkrqdarliivglfyetearkvcevykerlfgkkyvfwf 391
 QY 262 IGWYEDNWEYNLKAEGITCTVEOMRIAAEGHLLTTEALMWNONNOTTSGMTAEERHRL 321
 Db 392 igwyadnwfki--ydsinctvdeatveaghitteivmlnpantrsrsmcsqetvekl 449
 QY 322 NQALIEGYDINHRYPE---GYOEAPLAYDAVSWVALAFNAFKMTMBRLATTGKKSLRDTFT 378
 Db 450 tkrl-----krhpeetggfgeaplaydaivalalalnktsgggsgvrlfedfyn 500
 QY 379 DKEIADEIYAAMNSTQFLGVSQVAFSSQGDRIALTQTEQMTDGKYEKLYGTYDTOLDNIS 438
 Db 501 nqtitdqiyrannsssfegshvvdasgrmawtllieqlqggysykykgyydstckdlis 560
 QY 439 WLNTQEWIGKVPQDRTIVTHVRLTVSLPLFVCMCTISSCGIFVAFALIFINWKNHRV 498
 Db 561 wsktdkwlggspdaqtlviktrflsqklfsvsvslgslgvlavvcflsfnylnshvry 620
 QY 499 IQSSHPVQNTIMLVGIIICLISVILLIGDGRVSPPEEPKICQARAWLLSTGFTLAYGAM 558
 Db 621 iqnsqpnlnltavgcslalaavflgldyghiqnqpfvcqarllwllglfslgy9sm 680
 QY 559 FSKVWRVHRFTTK--AKTDPKKKVEPWKLYTWVSGLLSIDLVILLISWQTFDPLQRYLETF 616
 Db 681 ftklwwhtvftckeeekewrktlepkliyatvgtllvgmdvitlailwqldplhrtielf 740
 QY 617 PLEDVSTDDIKIRPELEHCSORNSMWLGVLVYGFKGLILVFGFLAYETRISIKVKOLN 676
 Db 741 akeepkedi-dvslpqlehcscskmmtwlgfygkglililgflayetsvstekln 799
 QY 677 DSRVYVGMSTYNNVWVLCITAPVGMVIAQQDASFAFVALAVFCFLSMLLIFVPKVIEV 736
 Db 800 dhravgmamynvavclitapvtmilsqqdaafaalaivfssyitlvilvfpkmrll 859
 QY 737 IRHP--KDKAESKYNPDSAISKEDERYQKLVTENEQRLRITQKEEKIRVLRQLVER 793
 Db 922 r 922

Db 860 itrgewqseqadtmktgssnnneeksrllekenrelekiiaekeervselrhqlqsr 918

AA28838

RESULT 10

ID AAY28838 standard; Protein: 961 AA.

AC AAY28838;

XX

DT 17-JAN-2000 (first entry)

XX

DE Human GABABR1a receptor protein.

XX

KW GABABR1a receptor protein; cloning; rat brain; GABABR2; GABAB receptor;

KW human gamma-aminobutyric acid receptor; metabotropic receptor; screening;

KW synaptic transmission; GABABR1b; cloned receptor; splice variant;

KW modulatory agent; molecular activity assay; antispastic; anti-addictive;

KW antineurodegeneration; analgesic; cardiovascular activity.

XX

OS Homo sapiens.

XX

PN WO9951636-A2.

XX

PD 14-OCT-1999.

XX

PF 02-APR-1999; 99WO-US07352.

XX

PR 03-APR-1998; 98US-0080676.

XX

PA (NPSF-) NPS PHARM INC.

PI Garrett JE, Simin RT, Busby JG, Stormann TM;

XX

DR WPI; 1999-610994/52.

XX

DR N-PSDB; AAX90920.

XX

PT Novel nucleic acids, used to screen for specific modulators, e.g. for

PT treating spasticity or Alzheimer's disease

XX

PS Disclosure; Fig 2A-2F; 78pp; English.

XX

CC The present sequence is GABABR1a receptor protein cloned from rat brain.

CC This is closely related to GABABR2. GABAB receptors are metabotropic

CC receptors that modulate synaptic transmission in brain. GABABR1a differs

CC from GABABR1b in that the N-terminal 147 residues are replaced by 18

CC amino acids. Both of these cloned receptors appear to be splice variants.

CC They are expressed in cells that express GABABR2. They are used to raise

CC antibodies to screen for specific modulators. These modulators have

CC antispastic, antineurodegeneration, analgesic, anti-addictive,

CC cardiovascular activities.

XX

SQ Sequence 961 AA;

Query Match 46.4%; Score 2030.5; DB 20; Length 961;

Best Local Similarity 49.3%; Pred. No. 2.6e-192;

Matches 384; Conservative 152; Mismatches 220; Indels 23; Gaps 8;

Qy 24 PHLQGVAGRPDE--LHIGGIPPIAGKGGWQGGACMPATRLALDDVKNPDLPGFKLI 81

Db ||| : : : ||| : ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

155 phcqvnrtpshserravvlgalfpms--ggwpgggacqpavemaledvnsrdilpdyelk 212

Qy 82 LHSNDSECPGLGAVMYNLLYNKPKLLAGCSVCTVAEAKMWNLLVLCYGASSP 141

Db ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : |||

213 lhhdsckopgatkyllyellndpdkllmpgcsstvtvaeearmwnllivsygssp 272

Qy 142 ALSDRKRFPFLRTPHSATVHNPTRIKMKFGWSVAILQQAEVEFISTVELENRCME 201

Db ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : |||

273 alsnrqrftfftrhpsatlhnptrvklfkqgwkkiaitqqttevtfstlddeerveke 332

Qy 202 AGVEIVTRQSFSDPTDAVRNLRQDARIIVGLFYVVAARRVLCEMYKQOYLGRAHWFF 261

Db ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : |||

333 agieitfqsfdsdpavpvknkrqdarliivgftearkvfcevykerlfgkkywfl 392

Qy 262 IGWYEDNMYEYNLKAEGITCTVEQMR1AAEGHLLTTEALMWNQNNQTTISSMTAEERHRL 321

Db ||| ||| : : : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : |||

393 igwyadnwfkj--ydpnsinctvdeanteaveghitteivmlnpantrsisnmsqsefvekl 450

Qy 322 NOALIEEGYDINHRYPE---GYEQAPLAYDAVWSVALAFNKTMERLTTGKSLRDFTTY 378

Db ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : |||

451 tkrl-----krhpeetggfqaeplaydaialalalnhts9999sgvrledfnyn 501

Qy 379 DKEIADEIYAAMNSTQFLGVSGVAFSSQGDRIATQIEQIDGKYEKIGGYDTDLNLS 438

Db : : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : |||

502 nqtitdqiyranssssfegvshvfdasgrmawllieqlg99sykkigydstkddls 561

Qy 439 WLNTQWITGGKVPQDRTIVTHVRVSLPLFVCMCTISSCGIFVAFALLIFINWKKHRRV 498

Db ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : |||

562 wsktdkwiggppadqtiwikfrfslsqklfsvslslgvlavvcisfnlyshvry 621

Qy 499 IQSSHPVCNTMLFCVVIICLISVILLGIDGRFVSPPEYKICQARAWLLSTGFTLAYGAM 558

Db ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : |||

622 ignsqpnlnitavgcslaaavfpldgdyhignrqfpvcqarlwlilgl9fslyg9sm 581

Qy 559 FSKVMRVHRTTK--AKTDPKKKVPKLYTMVSGLLSIDLVLLSQWIFDPLQRYLETF 616

Db ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : |||

682 ftkiwwhtvftkkeekewrktlepklyatvgllvgmdvltlaiqvldphrtietf 741

Qy 617 PLEDPVSTDDIKIRPELEHESQNSMMGLVYGFKLILVFGFLPLAYETRSIKVKQIN 676

Db ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : |||

742 akeepkedi-dvsilpqlehcscrkmtwlgifygklllllglflayetskstekln 800

Qy 677 DSRVYGMISYVNVVLCILITAPVGMVIAOODASFAFVALAVIFCCFLSMLLIFVPKVIEW 736

Db ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : |||

801 dhravgmalyinvavllclitapvmllssqgdaafasialvssyitlvivfvpkmrll 860

Qy 737 IRHP--KDKAESKYNPDSAISKEDERYQKLVTEQOLRITQKEEKIRVLQRQLVER 793

Db ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : |||

861 itrgewqseqadtmktgssnnneeksrllekenrelekiiaekeervselrhqlqsr 919

RESULT 11

AA29798

ID AAY29798 standard; Protein: 961 AA.

XX

AC AAY29798;

XX

DT 15-NOV-1999 (first entry)

XX

DE Human gamma-amino-butyric acid B receptor subunit GABABR1a.

XX

KW Gamma-amino-butyric acid B receptor subunit; HG20; GABABR1a;

KW depression; epilepsy; neuropsychiatric disorder; dementia;

KW muscular contraction; central nervous system disorder.

XX

OS Homo sapiens.

XX

PN WO9940114-A1.

XX

PD 12-AUG-1999.

XX

PF 03-FEB-1999; 99WO-US02361.

XX

PR 05-FEB-1998; 98US-0073767.

XX

PA (MERI) MERCK & CO INC

PA (MERI) MERCK FROSST CANADA INC.

PA (UYTE-) UNIV TEXAS HEALTH SCI CENT SAN ANTONI.

PA (USSH) US NAT INST OF HEALTH.

XX

PI Bonner TI, Bonnert TP, Clark J, Kolakowski LF, Liu Q;

PI McDonald T, Ng GYK;

XX

DR WPI; 1999-527300/44.

DR N-PSDB; AAZ06970.

XX

PT New DNA encoding human and murine receptor subunits, useful for
PT identifying agonists and antagonists for treatment of depression,
PT epilepsy and neuropsychiatric disorders
XX
XX
PS Claim 11; Fig 18; 128pp; English.

XX The present sequence represents a human gamma-amino-butyric acid (GABA)
CC B receptor (GABAR) subunit designated GABAR1A. The present invention
CC also describes the GABAR subunit designated HG20. Cells expressing
CC the new receptor subunits are useful for identifying GABAR agonists
CC and antagonists. HG20 proteins and their antagonists are useful for
CC inhibiting HG20 or GABAR function, useful for treating depression,
CC epilepsy, neuropsychiatric disorders, dementias, muscular contractions,
CC and central nervous system disorders.

XX Sequence 961 AA;

Query Match 46.4%; Score 2030.5; DB 20; Length 961;
Best Local Similarity 49.3%; Pred. No. 2.6e-192;
Matches 384; Conservative 152; Mismatches 220; Indels 23; Gaps 8;

QY 24 PHLOGVAGRPDE--LHIGGIFPIAGKGGWGGQACMPATRLALDDVKNKPNLLPGFKLI 81
DB 155 phcqvnrtpsherravvigaifpms--ggwpggacqavemaledvnsrrdlpdyelk 212
QY 82 LHSNDECEPGLGASVYNLYNKPQLMLLAGCSTVCTTVAEAAKMNWLVLCYGASSP 141
DB 213 lihhdskcdpgqatkylyellyndpikilmpgcssvstlvaeaaarmwlvlysgssp 272
QY 142 ALSDRKRPTLFRTHPSATVHNTRIKLMKFGWSRVAILQQAAEEVFISTVEDLENRCME 201
DB 273 alsnrgfrptftrhpsatlhnptrvklfekwgvkktiatiqgttevtstlddleervke 332
QY 202 AGVEIVTQSFSLDPTDAVNLRQDAIIVGLFVYVAARVLCMEVKQOLYGRAHWYFF 261
DB 333 agieifrgsfddpavpvnkrlrqdarilvlgfietearkvcevykerlfgkkywfl 392
QY 262 IGWYEDNWYEVNLEKAEICTVQMRTAAAGHLLTTEALMNQNNQTTISGMTAEFFHRL 321
DB 393 igwyadnwfkii--ydpisinctvdeataveghitteivmnpantrsisnmtsqefekl 450
QY 322 NQALIEGVDINDRPDE---GQEPAPLAYDAVMSVALAFNKNWERTTTGKKSRLDEFTYT 378
DB 451 tkrl-----krhpeetggfgeaplaydaiwalalanktsgggrsvrledfyn 501
QY 379 DKEIADIYAAMNSTOPLGSGVVAFSQGDRIALTOIEQMIDCKYELGYDTQLDNLS 438
DB 502 nqitqgiyramnsfsgvsgvfvdasgsrmaawtlieqiggykkgiydstkdcls 561
QY 439 WLNTQWIGGVQPDRTIVPHVLRVTSLPLFVCMCTISSGQIFVAFALIIFNIWNKHRRV 498
DB 562 wsktdkwgspadqtlviktfrlsqkifsvsvlssgvlavvclslfnylnshvry 621
QY 499 IQSHHPVCNTIMLFGVILICISLVLLIDGRFVSPPEYPKICQARWLLSTGFTLAYGAM 558
DB 622 iqsqpnlnlntavgcslalaavfplglgdyhigrnqfpvcqarlwlglgfslygysm 681
QY 559 FSKVWRVHRTTK--AKTDPKKKVEPKLTMVSGLLSIDLVILLSQIDPQLRYLETFF 616
DB 682 ftklwwhtvftkkekewrktlepklyatvgllvgmdvitalwqldpplrhtetf 741
QY 617 PLEDVPTSTDDIKIRPLEHCESSORNSMWLGLVYFGKGLIVLFGFLAYETRSIKVKQIN 676
DB 742 akeepkedi-dvslpqlehcscrkmtwlgfygkglllllgliflayekskvstekin 800
QY 677 DSRVGMISYVNVVLCILITAPVGMVIAQQDASPAFVALAVIFCCFLSMILLIFYPKVIEV 736
DB 801 dhravgmaiynvavclitapvtmilssqdaafafaslaivfssytilvlvfpkmrl 860
QY 737 IRHP--KDAESKNPDNSATSKDEERYQKLVNTENQLORLITOKEKIRVLRORLVER 793
DB 861 itrgewgseqdtkmktgssntnnneeksrlllekenrelekkiaeeervslrhlqsr 919

RESULT 12

AAV14101
ID AAV14101 standard; Protein; 961 AA.

XX AAV14101;

AC AAV14101;

XX 21-JUL-1999 (first entry)

DT Human GABAR receptor la protein sequence.

DE
XX GABAR receptor; gamma aminobutyric acid type B receptor; inhibitor;
KW transient lower oesophageal sphincter relaxation; spasticity; emesis;
KW gastro-oesophageal reflux disease; epilepsy; psychiatric disorder; TLESR;
KW irritable bowel syndrome; dyspepsia; arthritis; allergy; diagnosis;
KW autoimmune disease; neoplastic disease; infectious disease; therapy.

XX Homo sapiens.

OS W09921890-A1.

XX 06-MAY-1999.

XX 27-OCT-1998; 98WO-SE01947.

XX 17-JUL-1998; 98SE-0002575.

XX 27-OCT-1997; 97SE-0003914.

XX 16-MAR-1998; 98SE-0000864.

XX (ASTR) ASTRA AB.

XX Ekstrand J;

XX WPI: 1999-302985/25.

XX N-PSDB; AAX58054.

PT Polynucleotides encoding human and canine gamma aminobutyric acid
type B receptors, used to screen for compounds that are inhibitors
of transient lower oesophageal sphincter relaxations

PS Claim 17; Page 79-84; 222pp; English.

CC This sequence is a human gamma aminobutyric acid type B (GABAR)
receptor of the invention. Nucleic acid molecules encoding GABAR
receptors can be used to screen for compounds that are inhibitors of
transient lower oesophageal sphincter relaxations (TLESR). They can also
be used to screen for agonists or antagonists of the GABAR receptors.
Inhibitors of TLESR are useful for treating gastro-oesophageal reflux
disease. Other uses of GABAR receptors, such as human GABAR Ric or Id,
comprise diagnosis or treatment of conditions related to GABAR
dysfunction, e.g. epilepsy, psychiatric disorders, emesis, irritable
bowel syndrome, dyspepsia, spasticity, arthritis, allergies, autoimmune
diseases, neoplastic diseases, pain and infectious disease.

XX Sequence 961 AA;

Query Match 46.4%; Score 2030.5; DB 20; Length 961;
Best Local Similarity 49.3%; Pred. No. 2.6e-192;
Matches 384; Conservative 152; Mismatches 220; Indels 23; Gaps 8;

QY 24 PHLOGVAGRPDE--LHIGGIFPIAGKGGWGGQACMPATRLALDDVKNKPNLLPGFKLI 81

DB 155 phcqvnrtpsherravvigaifpms--ggwpggacqavemaledvnsrrdlpdyelk 212

QY 82 LHSNDECEPGLGASVYNLYNKPQLMLLAGCSTVCTTVAEAAKMNWLVLCYGASSP 141

DB 213 lihhdskcdpgqatkylyellyndpikilmpgcssvstlvaeaaarmwlvlysgssp 272

QY 142 ALSDRKRPTLFRTHPSATVHNTRIKLMKFGWSRVAILQQAAEEVFISTVEDLENRCME 201

DB 273 alsnrgfrptftrhpsatlhnptrvklfekwgvkktiatiqgttevtstlddleervke 332

```

QY 202 AGVEIVTRQSFSLSDPTDAVNRRLRODARIIVGLFYVVAARRVLCEMYKQOOLYGRAHVWFF 261
DB 333 agieitfrqsfdsdpavpvnkrlqrdariivglfyetearkvfcevykerlfgkkywfl 392
QY 262 IGWYEDNWYENLKAEGITCTVEQMRIAARGLHTTTEALMNNQNTTISGMTAEFRHRL 321
DB 393 igwyadnwfkii--ydpisinctvdeameveghitteivmlpnpantrsisnmtsgefevkl 450
QY 322 NQALIEEGYDINHRYPE---GYQEAPLAYDAVNSVALAFNKNKMERLTTGKKSRLDRFTYT 378
DB 451 tkrl-----krhpeetggfgeaplaydaivalalalnktsggggrsvrledfyn 501
QY 379 DREIADEIYAAMNSTQFLGSGVAVFSSQGDRIALTQIEQIDGKYELKGYDTQLDNLS 438
DB 502 nqtldqiyramnsssfegsvghvfdasgrmawtllieqlggsykkigydstckdls 561
QY 439 WLNTEQWIGKVPQDRTIVTHVLRVSLPLFVCMCTISSCGIFVAFALIIIFNIWNKHRRV 498
DB 562 wsktdkwigspadqtlviktfrfisklfisvslssglvavvcisfniynshvry 621
QY 499 IQSSHPVCNTIMLFGVITCLISVILLGIDGRFVSPPEYKPKICQARAWLLSTGFTLAYGAM 558
DB 622 iqnsqpnlnltavgsalaaavfplgdghyhgirnqfpvcqarlwlglgfslygsm 681
QY 559 FSKVVRVHRFTTK--AKTDPKKVPEWKLTYTWVSGLLSIDLVILLSSQIFDPLQRYLETF 616
DB 682 ftkiwwhvftkceekewrklepkiyatvgllvgmdvltalwqivdpjhrtleft 741
QY 617 PLEDPVSTDDIKIRPELHESORSNMLGVYGRFKLILVGLFLAYETRSIKVKQIN 676
DB 742 akepekdi-dvslpqlehcscrkmtwlgifygkglililgifyecksvstekin 800
QY 677 DSRVYGMSTYNNVVLCLITAPVGMVIAQODASFAFVALAVIFCCFLSMLLIIFVPKVIEW 736
DB 801 dhraqvmalynvavclitapvtmilssqqdaafaslaivfssyitlvlfvpkmrl 860
QY 737 IRHP--KDKAESKYNPDSAISREDEERYOKLVTENQOLRLITQEKIRVLRORLVER 793
DB 861 itrgewqseaqdmtkgsntnnneeksrillekenrelekliaaekearvselrhqlqsr 919

RESULT 13
AAAY49133
ID AA49133 standard; Protein; 1323 AA.
AC AA49133;
XX 07-JAN-2000 (first entry)
XX GABA-BR1a*Gqo5 fusion construct protein sequence.
XX G-protein fusion receptor; CaR; calcium receptor; GluR; head injury;
KW metabotropic glutamate receptor; GABAR; chimeric receptor; stroke;
KW gamma-aminobutyric acid receptor; allosteric modulator; antagonist;
KW spinal cord injury; epilepsy; ischaemia; hypoglycaemia; anoxia;
KW Alzheimer's disease; hyperparathyroidism; osteoporosis; depression;
KW cognitive disorder.
XX Homo sapiens.
XX WO951641-A1.
XX 14-OCT-1999.
XX 02-APR-1999; 99WO-US07333.
XX 03-APR-1998; 98US-0080671.
XX (NPS- ) NPS PHARM INC.
XX Stormann TM, Hammerland LG, Storjohann LL, Busby JG, Garrett JE,
PI Simin RT;

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XX WPI: 1999-610995/52.
XX N-PSDB; AAZ31064.
XX New G-protein fusion receptors and chimeras containing domains from
PT different receptors, used to screen for modulators, potentially useful
PT e.g. for treating or preventing stroke or Alzheimer's disease -
XX Disclosure; Fig 14; 255pp; English.
XX The invention relates to G-protein fusion receptors (I) comprising:
CC (1) in the N to C direction, extracellular (ECD), transmembrane (TMD) and
CC intracellular (ICD) domains, each chosen independently from a CaR
CC (calcium receptor), GluR (metabotropic glutamate receptor) and GABAR
CC (gamma-aminobutyric acid receptor); (2) an optional linker attached to
CC the C-terminus of ICD; and (3) a G-protein (GP) linked to ICD or the GP
CC linker. (I), and recombinant chimeric receptors (CR) without the GP
CC component, are used to assess function of the various domains and to
CC identify compounds (e.g. allosteric modulators or antagonists) that act
CC on these domains. The modulators are potentially useful for treating or
CC preventing diseases associated with the receptors, e.g. stroke, head or
CC spinal cord injury, epilepsy, ischaemia, hypoglycaemia, anoxia,
CC Alzheimer's disease, hyperparathyroidism, osteoporosis, cognitive
CC disorders and depression. Nucleic acid (II) that encodes (I) is used:
CC (1) for recombinant production of corresponding proteins; and (2) to
CC produce cells used in screening for modulators. Use of CaR and mGluR
CC domains allows presentation of GABAR domains, to a binding agent, in a
CC form more like the natural domain structure compared with use of
CC incomplete receptors, lacking one or more domains. By shuffling different
CC domains, agents can be identified that affect particular domains of a
CC receptor.
XX Sequence 1323 AA;
XX
Query Match 46.4%; Score 2030.5; DB 20; Length 1323;
Best Local Similarity 49.3%; Pred. No. 4.4e-192;
Matches 384; Conservative 152; Mismatches 220; Indels 23; Gaps 8;
QY 24 PHLGGVAGRDE--LHTGGIFPIAGKGWGGQACMPATRLALDDVKNQPNLLPGFKLI 81
DB 155 phcvnrtpsherravyigalfpms--ggwpgggccqcpavemaledvnsrrdildpylek 212
QY 82 LHSNDSCEPGLGASVMYNLLYNRPQKRLMLLAGCSTVCTTVAEAAKMWNLIYLCYASSP 141
DB 213 lihdsckdpgatkyllyellyndpikilimpqcssvstlvaearmwnlilvlysgsssp 272
QY 142 ALSDRKRPTLFRTHPSATVHNPRIKLMKFGWGRVAILQQAEEVFISTVEDLENRCME 201
DB 273 alsnrqrfptfrthpsatlhnptrvklfegwkgtkatiqqttevtstldleervke 332
QY 202 AGVEIVTRQSFSLSDPTDAVNRRLRODARIIVGLFYVVAARRVLCEMYKQOOLYGRAHVWFF 261
DB 333 agieitfrqsfdsdpavpvnkrlqrdariivglfyetearkvfcevykerlfgkkywfl 392
QY 262 IGWYEDNWYENLKAEGITCTVEQMRIAARGLHTTTEALMNNQNTTISGMTAEFRHRL 321
DB 393 igwyadnwfkii--ydpisinctvdeameveghitteivmlpnpantrsisnmtsgefevkl 450
QY 322 NQALIEEGYDINHRYPE---GYQEAPLAYDAVNSVALAFNKNKMERLTTGKKSRLDRFTYT 378
DB 451 tkrl-----krhpeetggfgeaplaydaivalalalnktsggggrsvrledfyn 501
QY 379 DREIADEIYAAMNSTQFLGSGVAVFSSQGDRIALTQIEQIDGKYELKGYDTQLDNLS 438
DB 502 nqtldqiyramnsssfegsvghvfdasgrmawtllieqlggsykkigydstckdls 561
QY 439 WLNTEQWIGKVPQDRTIVTHVLRVSLPLFVCMCTISSCGIFVAFALIIIFNIWNKHRRV 498
DB 562 wsktdkwigspadqtlviktfrfisklfisvslssglvavvcisfniynshvry 621
QY 499 IQSSHPVCNTIMLFGVITCLISVILLGIDGRFVSPPEYKPKICQARAWLLSTGFTLAYGAM 558

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Db 622 iqnsqpnlnltavqcsalaaavfplgldgylhgrnqpfvccqarlwlglglslygysm 681
QY 559 FSKVWRVHRTTK--AKTDPKKKVEPWKLYTMVSGLLSIDVLVLLSWQIFDPQLRYLETF 616
Db 682 ftklwwhtvftkkekewrktlepklyatvgllvgmdvltaiwqldvplhrtietf 741
QY 617 PLEDVSTDDIKTRPELEHCESQNSWGLVYGFKGLIIVFGLFLAYETRSIKVKQIN 676
Db 742 akeepkedi-dvslplqlncssrkmntwlgfygkgllllglflayeksvstekin 800
QY 677 DSRVGVSIYNNVVLCLITAPGVGVIAQQDASFAFVALAVIFCCFLSMLLIFVPKVEV 736
Db 801 dhravgmaynvavclitapvtmllssqdaafafaslaivfssytlvlfvpmkrrl 860
QY 737 IRHP--KDKAESKNPDSAIKDEERYQKLVTENEQLRLITQKEEKIRVLRQLRVER 793
Db 861 itrgewqseqdmtkgtssntnnneeksrlllekenrelekliaeeervselrhqlqsr 919

RESULT 14
AAW40117
ID AAW40117 standard; Protein: 793 AA.
AC AAW40117;
DT 03-JUN-1998 (first entry)
DE Human GABA-BR1a/b receptor protein.
KW Gamma-aminobutyric acid; GABA-BR1a/b receptor; human; brain; agonist;
KW inhibitory neurotransmitter; peripheral nervous system; antagonist;
KW treatment; dementia; depression; anxiety; bronchial inflammation; asthma;
KW epilepsy; cognitive function.
XX Homo sapiens.
XX OS WO9746675-A1.
PN 11-DEC-1997.
PD 19-MAR-1997; 97WO-EP01370.
PF 22-NOV-1996; 96US-0756091.
PR 30-MAY-1996; 96US-0655716.
XX (NOVS ) NOVARTIS AG.
XX PA Bettler B, Bittiger H, Froestl W, Kaupmann K, Mickel SJ.
XX PI WPI; 1998-042183/04.
XX DR N-PSDB; AAV10265.
XX PT Purified GABA-B receptor or receptor protein - and antagonists of
XX these which may be useful in treating nervous system disorders
XX Claim 4; Page 62-67; 108pp; English.
XX This sequence represents a novel human GABA-B receptor protein,
XX GABA-BR1a/b. GABA (gamma-aminobutyric acid) is the major inhibitory
XX neurotransmitter found in the brain and peripheral nervous system
XX and this receptor may be used for the identification of GABA-B
XX receptor agonists and antagonists. Such proteins may be used in
XX treatment of dementia, depression, anxiety, epilepsy, spasticity,
XX bronchial inflammation or asthma or to improve cognitive function.
XX GABA-B receptor ligands and probes derived from this sequence can be
XX used to assay for GABA-B receptors or DNA encoding them.
XX Sequence 793 AA;

Query Match 46.4%; Score 2029.5; DB 19; Length 793;
Best Local Similarity 49.9%; Pred. No. 2.4e-192;
Matches 381; Conservative 151; Mismatches 211; Indels 21; Gaps 7;

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QY 37 LHIGFIPTAGKGWGGQACMPATRLALDDVKNQPNLLPGFKLILHSNDSECEPGLGAS 96
Db 2 vyigalfpms--gwpvggqacpavemaledvnsrrldilpdyelkllhdsckdpgatk 59
QY 97 VMYNLLYKPKQLMLLAGCSTVCTTVAEAAKWNLLVLCYGASSPALSDDKRPPTLFRTH 156
Db 60 yiyellyndpklilimpccssvstlvaearmwnllivsygsspsalsnqrifptfrth 119
QY 157 PSATVHNPTRIKLMKFGMSRVAILQQAAEEVFISTVEDLENRMEAGVELVTRQSLSDP 216
Db 120 psathmpttrvlfekwggwkkiatqqttevfstlddleervkeagietfrqsfpsdp 179
QY 217 TDAVRLNRQDARIIVGLFVYVAARVLCEMYKQQLYGRAHVFIFGWEDNNMYENLKA 276
Db 180 avpvknlkrqdarilvglyetearkvfcevkykerlfgkkyvfwlgyadnwfk1--yd 237
QY 277 EGITCTVQDMRTAAEGHLTTEALMNQNNQTTISGMTAEFRHRLNQALIEEGYDINHDR 336
Db 238 psinctvdemteaveghitteilvminpantrsisnmtsdfekltkr1-----kr 288
QY 337 YPE---GYQEAFLAYDAVMSVALAFNKTWERLTGKKSLRDTFTYDKETADEIYAAMNST 393
Db 289 hpeetggfgeaplayadaiwalalanktsggggrsvrlfednynqttldqlyramss 348
QY 394 QFLGVGVVAFSSQGDRIALTQIEQMIDGKYEKLYGYDTQDLNLSMLNTEQWIGKVPQD 453
Db 349 sfegvsgvhdafsgsrmawtliedlqggsgykyggydstkddlskwtckdwiggspad 408
QY 454 RTIVTHVLRTVSLPFLVCMCTISSGIFVAFALIIIFNIWKNHRRVITQSSHPVCNTIMLFG 513
Db 409 qtlviktfrfksqklfifsvsvissigivlavvclslfniynshvryiqnsgpnlmnavg 468
QY 514 VIICILSVTLGIDGRFVSPPEYKPCIOARAWLLSTGFTLAYCAMESKVMVRVHRFTTK-- 571
Db 469 csialaavfplgldgylhgrnqpfvccqarlwlglglslygysmftkikiwwhtvftk 528
QY 572 AKTDPKKKVEPWKLYTMVSGLLSIDVLVLLSWQIFDPQLRYLETFPDPVSTDDIKIR 631
Db 529 ekewrktlepklyatvgllvgmdvltaiwqldvplhrtietfakeepkedi-dvsl 587
QY 632 PELEHCESQNSWGLVYGFKGLIIVFGLFLAYETRSIKVKQINDSRVYSGMSIYNNVVL 691
Db 588 pqlehcscrkmtwlgfygkgllllglflayeksvstekinhdravgmaynvavl 647
QY 692 CLITAPGVGVIAQQDASFAFVALAVIFCCFLSMLLIFVPKVEVIRHP--KDKAESKN 749
Db 648 clitapvtmllssqdaafafaslaivfssytlvlfvpmkrrlitrgewqseqdmtk 707
QY 750 PDSAIKDEERYQKLVTENEQLRLITQKEEKIRVLRQLRVER 793
Db 708 tgsstnnneeksrlllekenrelekliaeeervselrhqlqsr 751

RESULT 15
AAV14109
ID AAV14109 standard; Protein: 892 AA.
XX AAV14109;
AC AAV14109;
XX 21-JUL-1999 (first entry)
XX Human GABAB receptor 1g protein sequence.
XX GABAB receptor; gamma aminobutyric acid type B receptor; inhibitor;
XX transient lower oesophageal sphincter relaxation; spasticity; emesis;
XX gastro-oesophageal reflux disease; epilepsy; psychiatric disorder; TLESR;
XX irritable bowel syndrome; dyspepsia; arthritis; allergy; diagnosis;
XX autoimmune disease; neoplastic disease; infectious disease; therapy;
XX alternative splicing; isoform.
XX Homo sapiens.

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